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EP 1 074 617 A2

- F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420
- 5 F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//Hs.147802:R71297
- 10 F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172
- F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248
- 15 F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284
- 20 F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017
- F-HEMBA1001099
- 25 F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4-61:341:85//Hs.5247:AF029750
- F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497
- 30 F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940
- 35 F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917
- F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747
- 40 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341
- 45 F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582
- F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457
- 50 F-HEMBA1041174//ESTs//1.4e-63:363:92//Hs.132798:AA922226
- 55 F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//5.0e-54:555:71//Hs.55165:AA573499
- F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463

EP 1 074 617 A2

P-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717

5 F-HEMBA1001226//ESTs/1.9e-11:407:65//Hs.157977:AI369694

F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748

10 F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058

F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046

15 F-HEMBA1001265

F-HEMBA1001281

20 F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155

F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-30:530:64//Hs.154050:AC004131

25

F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741

30 F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs.155464:AF088219

35 F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:AI129590

F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201

40

F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873

45 F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301

F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:L20861

50

F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108734:AI073427

55

F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013

EP 1 074 617 A2

F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569

5 F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA,
complete cds//3.6e-105:516:97//Hs.9006:AF057358

F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794

10 F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425 :AI198074

F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156

15 F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353

F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-
20 132:643:97//Hs.124217:AA020848

F-HEMBA1001388

25 F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660

F-HEMBA1001398

30 F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117

F-HEMBA1001407//ESTs//10.53:390:57//Hs.150447:AI017798

35 F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108

F-HEMBA1001413

40 F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605

F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040

45 F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726

F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible),
polypeptide 2//1.2e-74:469:80//Hs.1361:M55053

50 F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031

F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//6.8e-47:
55 550:71//Hs.55165:AA573499

F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIPA1) mRNA, complete
cds//0.82:312:58//Hs.7019:AB005666

EP 1 074 617 A2

- F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107
- 5 F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412
- F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:88//Hs.40100:AB002390
- 10 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489:99//Hs.14409:AB011144
- 15 F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451
- F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219
- 20 F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054
- F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-105:773:82//Hs.23094:M19503
- 25 F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902
- 30 F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869
- F-HEMBA1001526
- 35 F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476
- F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580
- 40 F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652
- F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205
- 45 F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814
- F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:AJ012449
- 50 F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184
- 55 F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228
- F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:

EP 1 074 617 A2

64//Hs.115778:D79988

5 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:
78//Hs.90998:D50918

F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210

10 F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400

F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870

15 F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!
[H.sapiens]//0.038:198:64//Hs.34579:AI338536

20 F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899

F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:
61//Hs.79706:U53204

25 F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560

F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283

30 F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121

F-HEMBA1001661

35 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA,
complete cds//7.9e-146:669:99//Hs.107254:AC005943

40 F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-
57:447:79//Hs.158095:AB007953

F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788

45 F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060

F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760

50 F-HEMBA1001709//EST//0.85:131:65//Hs.131451:AI023995

F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:AI302836

55 F-HEMBA1001712//EST//0.26:214:59//Hs.159088:AI383114

F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL

EP 1 074 617 A2

PRECURSOR [Rattus norvegicus]//3.0e-30:195:92//Hs.132948:AA194452

F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554

5

F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101524:U58197

10

F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363

F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415

15

F-HEMBA1001744//EST//8.7e-77 :420:92//Hs.133226:AI052250

F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37:300:62//Hs.10887:AB013924

20

F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328

F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//0.76:218:60//Hs.135553:N41598

25

F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//Hs.98776:AC005622

30

F-HEMBA1001784//Homo sapiens mRNA for KJAA0474 protein, complete cds//6.4e-09:265:67//Hs.158232:AB007943

35

F-HEMBA1001791

F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570

40

F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817

F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.8e-07:439:59//Hs.266:U06233

45

F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//2.-5e-175:809:98//Hs.118164:AB007969

50

F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305

F-HEMBA1001815

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F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//4.9e-80:842:70//Hs.158174:U66561

EP 1 074 617 A2

F-HEMBA1001820//EST//0.057:214:62//Hs.148715:A1223845

5 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//6.7e-42:510:65//Hs.66392:AF064244

10 F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//5.2e-13:253:68//Hs.85313:AF071309

F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//Hs.6151:D87078

15 F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.155243:N70293

F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:68//Hs.6833:AB002324

20 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.8e-185:865:98//Hs.78946:AB014517

25 F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121

30 F-HEMBA1001866//ESTs. Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:AI141922

35 F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:367:95//Hs.15423:T84036

F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//5.4e-86:835:76//Hs.158095:AB007953

40 F-HEMBA1001896

F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//0.43:114:71//Hs.6133:U94346

45 F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633

50 F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:200:62//Hs.9573:AF027302

F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511

55 F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141

EP 1 074 617 A2

F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:855:99//Hs.154934:AF000145

5 F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295

F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221

10 F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882

F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943

15 F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360

F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.30:85:69//Hs.25674:AF072242

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F-HEMBA1001962//ESTs//0.0012:289:59//Hs.125492:AA938930

F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708

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F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178

30

F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732

35 F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100

F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581

40

F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) //9.8e-09:294:63//Hs.99936:X14487

45

F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803 :W63582

F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867:M93426

50

F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907

55

F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827

F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057

EP 1 074 617 A2

F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]/4.5e-26:223:81//Hs.105292:AA504776

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F-HEMBA1002084

F-HEMBA1002092

10

F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA,
complete cds//5.6e-21:124:96//Hs.101842:L32832

15

F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]/5.9e-09:434:
62//Hs.135102:AI190276

F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973

20

F-HEMBA1002119

F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802

25

F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393

F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:
D86980

30

F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:
62//Hs.23741:AB018263

35

F-HEMBA1002151

F-HEMBA1002153//EST/10.014:328:60//Hs.149115:AI244695

40

F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-
49:303:79//Hs.158241:AB007976

45

F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:
67//Hs.929:M57965

F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:
AJ007590

50

F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:
AF088219

55

F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:
AF026245

EP 1 074 617 A2

- F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141
- 5 F-HEMBA1002189//EST//5.1 e-24:193:81//Hs.163161:AA778363
- F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.27:382:59//Hs.21992:AB014589
- 10 F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs.159897:AB007970
- 15 F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696
- F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767
- 20 F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.59906:AA001281
- F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs.67619:AB007957
- 25 F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394
- 30 F-HEMBA1002237//EST//0.044:1 37:66//Hs.144448:AA812455
- F-HEMBA1002241
- 35 F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887
- F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936
- 40 F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420
- 45 F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//1.0:395:60//Hs.150926:AF017445
- F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404
- 50 F-HEMBA1002321//Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds//0.17:338:60//Hs.77729:AB010710
- 55 F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982
- F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:

EP 1 074 617 A2

D42087

5 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314

F-HEMBA10023481/EST//1.0e-19:285:70/Ms.121860:AA776692

10 F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996

F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:872:99//Hs.119023:AF092563

15 F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216

F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144

20 F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954

25 F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141

30 F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U79289

35 F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561

F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121:W26490

40 F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160

45 F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783

F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912

50 F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508

55 F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:83//Hs.6189:AB011133

F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235

EP 1 074 617 A2

F-HEMBA1002495

5 F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161

F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:
X98173

10

F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:
83//Hs.113283:AF018080

15 F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.Oe-
159:738:98//Hs.6764:AJ011972

20 F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795

F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951

25 F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-
46:238:87//Hs.10458:AF088219

F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:
98//Hs.68900:AF016903

30

F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:
U31875

35 F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:
57//Hs.20912:AB012162

40 F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205

F-HEMBA1002561//Humanclone 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:
U90905

45 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-
142:457:99//Hs.151411:AF075587

50 F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete
cds//2.8e-30:156:100//Hs.32170:AB015132

F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159

55 F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363

F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:

EP 1 074 617 A2

99//Hs.20141:AB011169

F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013

5

F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:AB018351

10

F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334

15

F-HEMBA1002629//Human density enhanced phosphatase 1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:U10886

F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390

20

F-HEMBA1002651

F-HEMBA1002659//Human vascular endothelial growth factor related protein VRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142

25

F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094:M19503

30

F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497

F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368

35

F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha) //0.00096:418:61//Hs.1323:S42457

40

F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.8e-11:541:601//Hs.124161:AF065164

45

F-HEMBA10026961//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647:AC004221

F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924

50

F-HEMBA1002712

F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800

55

F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521

EP 1 074 617 A2

F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811 :AB007867

5 F-HEMBA1002742//EST//0.97:138:60//Hs.160545:71596

F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061: X59372

10

F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806: AA018786

15 F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817

F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834: 98//Hs.74750:AB011126

20

F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833: AI299947

25 F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809

F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392

30

F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326

F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756

35

F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938

F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169: 820:97//Hs.28307:AF071185

40

F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744

45 F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733: 89//Hs.6059:AF093119

F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:M279904

50

F-HEMBA1002833

F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550

55

F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823

EP 1 074 617 A2

F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730

5 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AE79429

F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679

10 F-HEMBA1002921

F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001

15 F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915

F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148

20

F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053

25 F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703

30 F-HEMBA1002944//Human putative endothelin receptor type B-like protein mRNA, complete cds//0.83:326:58//Hs.27747:U87460

F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.26762:AA913925

35 F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099

F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092

40 F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828

F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219

45 F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)//1.5e-37:247:89//Hs.188:L20971

50 F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.7e-05:797:58//Hs.50758:AF092564

F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525

55 F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs.155464:AF088219

EP 1 074 617 A2

F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486

5 F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:330:78//Hs.113283:AF018080

F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.159425:AJ001454

10 F-HEMBA1003037//EST//0.53:59:74//Hs.148011:M268003

15 F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:337:95//Hs.I05907:AA186514

F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182

20 F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438

F-HEMBA1003067

25 F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164

30 F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865

F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454

35 F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461

F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881

40 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721

45 F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.musculus]//0.98:216:61//Hs.97865:AA405872

F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721

50 F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802

F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575

55 F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314

EP 1 074 617 A2

F-HEMBA1003136

F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279

5

F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670

10

F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.I41874:AB014588

F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740

15

F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs.II8831:AA211895

20

F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523

F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135

25

F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412

F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:154:85//Hs.113283:AF018080

30

F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765

F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784

35

F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310

F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012

40

F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.00054:432:58//Hs.I32206:AF039694

45

F-HEMBA1003250

F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64//Hs.49585:AF075292

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F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991

F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020

55

F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864

EP 1 074 617 A2

F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867

5 F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase
mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662

10 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.6e-167:799:
98//Hs.12836:AB011109

F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912

15 F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160

F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.105486:AA521012

20 F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete
cds//1.5e-189:865:99//Hs.124224:AB001872

25 F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:
X99459

F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254

30 F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328

F-HEMBA1003330

35 F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:
78//Hs.146395:AB002329

40 F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240,
R30272 and R28549 containing the EKLF, GCDH, CRTCL, and RAD23A genes, genomic
sequence//0.37:187:65//Hs.80265:AD000092

F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159

45 F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819

F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637

50 F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017

F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552

55 F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488

F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813

EP 1 074 617 A2

- 5 F-HEMBA1003403//Adducin 2 (beta) {alternative products }//5.0e-05:445:61//Hs.90951:U43959
- F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309
- 10 F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546
- F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962
- 15 F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:686:99//Hs.25812:AF058696
- 20 F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60//Hs.47822:AB002378
- F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08:775:58//Hs.3847:U59632
- 25 F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578
- 30 F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16:321:60//Hs.13999:AB014600
- F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443
- 35 F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:78//Hs.22271:D26067
- 40 F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811
- F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5.0e-75:736:73//Hs.505:U07559
- 45 F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311
- F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6e-33:562:64//Hs.81469:U01833
- 50 F-HEMBA1003556
- 55 F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122
- F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327

EP 1 074 617 A2

F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0e-58:455:66//Hs.101448:U35113

5 F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972

F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546

10 F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:108:99//Hs.18420:AA599232

15 F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:92//Hs.57937:W68285

F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405

20

F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827

25 F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916

F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782

30 F-HEMBA1003617//Homo sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344

35 F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:AF077954

F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750

40 F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159

F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591

45

F-HEMBA1003640//ESTs//1.1e-11:267:661//Hs.34359:AI122791

50 F-HEMBA1003645

F-HEMBA1003646

55 F-HEMBA1003656

F-HEMBA1003662

EP 1 074 617 A2

F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381

F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906

5

F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204

10

F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//1.6e-100:478:98//Hs.118866:AI017072

15

F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691

F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187

20

F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254:62//Hs.32316:AB011116

F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995

25

F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760

30

F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//Hs.91916:AF035317

F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921

35

F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839

F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102:753:81//Hs.23094:M19503

40

F-HEMBA1003742//Homo sapiens chromosome 19, cosmid

R31180//0.16:242:62//Hs.153325:AC005390

45

F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946

50

F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//Hs.8136:U81984

F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920

55

F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//1.7e-24:224:81//Hs.18171:AA524327

EP 1 074 617 A2

F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172

F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064

5

F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.13:222:61//Hs.89230:AF031815

10

F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239

F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:M88108

15

F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721

F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3e-85:586:87//Hs.6051:AB014516

20

F-HEMBA1003836//EST//6.8e-06:98:74//Hs.I45447:AI204220

25

F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.8e-40:151:88//Hs.139007:H74314

F-HEMBA1003856//ESTs//8.6e-53:286:95//Hs.116645:AI005167

30

F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66//Hs.21355:AB002367

35

F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.3e-30:580:63//Hs.27621 :U52840

F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.89563:D32002

40

F-HEMBA1003880

F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2e-18:302:67//Hs.23711:AB018295

45

F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.2e-49:295:92//Hs.114673:W72675

50

F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236

F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.081:345:58//Hs.78494:AB011097

55

F-HEMBA1003926//EST//2.5e-32:253 :83//Hs.132635:AI032875

EP 1 074 617 A2

F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:69//Hs.154668:AB002389

5 F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562

F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]//0.0029:222:61//Hs.144236:W52380

10

F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055

15 F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:66//Hs.2076:M29580

F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.1e-44:243:76//Hs.91146:N73230

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F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567

F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI138965

25

F-HEMBA1003978

F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009

30

F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456

35 F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//0.022:349:58//Hs.104640:AF000561

F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468

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F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493

F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573

45

F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:AI379721

F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.2e-51:359:84//Hs.15519:AB018315

50

F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:AI239930

F-HEMBA1004042//EST//0.00088:272:61//Hs.155763:AI312281

55

F-HEMBA1004045//EST//2.7e-20:408:66//Hs.162529:AA584160

EP 1 074 617 A2

- F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M60315
- F-HEMBA1004049//ESTs//8.1e-68:430:86//JHs.146307:AA584638
- 5 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457:58//Hs.82837:L13435
- 10 F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.5e-46:199:80//Hs.46328:D87942
- F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426
- 15 F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107
- F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M28713
- 20 F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.3e-39:335:79//Hs.46468:U45984
- 25 F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610:61//Hs.80712:D86957
- F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064
- 30 F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:AI419759
- F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.00055:343:62//Hs.5923:X82260
- 35 F-HEMBA1004143
- 40 F-HEMBA1004146
- F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI186056
- 45 F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.8e-15:591:60//Hs.159277:AB018341
- F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649:97//Hs.59988:AF067855
- 50 F-HEMBA1004199
- 55 F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:AI375427
- F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea

EP 1 074 617 A2

mays//1.2e-35:205:94//Hs.10092:AI189282

F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040

5

F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748

F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514

10

F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans]//0.012:156:67//Hs.I63588:AI073878

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F-HEMBA1004238

F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571

20

F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522

F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds//1.1e-28:295:72//Hs.56205:U96876

25

F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553:60//Hs.83634:U52112

30

F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.9e-73:490:77//Hs.141874:AB014588

F-HEMBA1004272

35

F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444

F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118:65//Hs.155313:AB002331

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F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.0:364:56//Hs.118738:AB018343

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F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.9e-187:868:99//Hs.101766:AF022795

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F-HEMBA1004289

F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484

55

F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:AI270047

F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:AI336314

EP 1 074 617 A2

F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452:65//Hs.69740:
 U09367
 5
 F-HEMBA1004323//EST//0.44:134:64//Hs.145464:AI204532
 F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.017:209:
 10 64//Hs.43627:U35612
 F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062
 15 F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888
 F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.49:80:
 20 73//Hs.139648:AB014606
 F-HEMBA1004341
 F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//2.7e-39:
 25 270:86//Hs.80686:D89667
 F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3e-46:190:
 30 92//Hs.27424:U75968
 F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.3022:D85376
 F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog
 35 [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928
 F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800
 40 F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019
 F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250
 45 F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818
 F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199
 50 F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin.
 [H.sapiens]//1.4e-20:144:88//HS.121076:AI246426
 F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay
 55 phenotype included)//4.8e-18:248:72//Hs.69747:M35531
 F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:

EP 1 074 617 A2

AF088219

5 F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080

F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606

10 F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984

F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450

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F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600

F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431

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F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-89:758:76//Hs.23094:M19503

25 F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans]//1.4e-61:296:99//Hs.114622:AA693492

30 F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800

F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:X53416

35

F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381

F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552

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F-HEMBA1004554

F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331

45

F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802

50 F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:AA479825

F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1 e-35:337:78//Hs.78160:AF010238

55

F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661

F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA,

EP 1 074 617 A2

complete cds//0.42:186:66//Hs.84136:1170370

5 F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606

F-HEMBA1004617//EST//0.027:188:61//Hs.I59094:AI383198

10 F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178

F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416

15 F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891

F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780

20 F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522

F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083

25 F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796

F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582

30 F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141

F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252

35 F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.64:313:
61//Hs.118578:X80821

40 F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:
73//Hs.155174:AB007892

F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515

45 F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:
X55019

50 F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:
60//Hs.68900:AF016903

55 F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:
70//Hs.116874:AA524909

F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515

EP 1 074 617 A2

F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004

5

F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503

10

F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813

F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504

15

F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626

20

F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.I53563:AF011333

F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082

25

F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060

30

F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.I55657:M61120

F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-115:909:78//Hs.23094:M19503

35

F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139

40

F-HEMBA1004771

F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235

45

F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106

F-HEMBA1004795

50

F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952

F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971

55

F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042

EP 1 074 617 A2

- F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646
- 5 F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481
- F-HEMBA1004847//ESTs//2.1 e-09:66:98//Hs.158161:AA312511
- 10 F-HEMBA1004850//EST//0.033:253:64//Hs.158782:A376601
- F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150
- 15 F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987
- 20 F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077
- F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633
- 25 F-HEMBA1004889//Growth arrest-specific I//0.20:146:68//Hs.65029:L13698
- F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304
- 30 F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106
- F-HEMBA1004918//EST//0.78:122:61//Hs.I45491:AI254348
- 35 F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172
- F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947
- 40 F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959
- F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331
- 45 F-HEMBA1004934
- 50 F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981
- F-HEMBA1004954//ESTs//0.0i4:404:60//Hs.11177:AA417813
- 55 F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478
- F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274

EP 1 074 617 A2

F-HEMBA1004972

5 F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:
58//Hs.154139:AB007914

10 F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946

F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013

15 F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750

F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589

20 F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026

F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429

25 F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:
72//Hs.151887:AF053356

30 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:
98//Hs.31921:AB014548

F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:
65//Hs.6727:AB014560

35 F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN
CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237

40 F-HEMBA1005039//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:
89//Hs.103948:K00627

45 F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete
cds//0.078:442:59//Hs.100602:AF010193

F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802

50 F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462

F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2)
mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587

55 F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:
57//Hs.27590:AB002381

EP 1 074 617 A2

F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785

5 F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105

10 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561

F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916

15 F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304

20 F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106

F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875

25 F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021

F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216

30 F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914

F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197

35 F-HEMBA1005202

F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436

40 F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547

F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081

45 F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302

F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399:79//Hs.129735:AF010144

50 F-HEMBA1005244//ESTs//2.5e-14:85:10011Hs,128744:AI191922

F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896

55 F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705:98//Hs.72660:AB011157

EP 1 074 617 A2

F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380

F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777

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F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//Hs.12451:U97018

10

F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232

F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs.155464:AF088219

15

F-HEMBA1005311

F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516

20

F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615

F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117

25

F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310:63//Hs.111597:U68723

30

F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:97//Hs.29361:AJ007581

F-HEMBA1005353//EST//5.4e-09:2-22:68//Hs.119508:AA485732

35

F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88//Hs.151689:U09414

40

F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572:73//Hs.43265:AF071787

F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905

45

F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs.154069:U06452

50

F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI93053

F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448

55

F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans]//1.0e-130:620:98//Hs.108990:N25951

EP 1 074 617 A2

F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans]//7.7e-151:727:97//Hs.17118:AI033807

5 F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513

F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347

10 F-HEMBA1005411

F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248

15 F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323

F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259:72//Hs.89897:U28687

20 F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783

F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107

25 F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:L37368

30 F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481:92//Hs.23094:M19503

35 F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219

F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:AF039694

40 F-HEMBA1005497//Glucocorticoid receptor alpha { alternative products}//8.7e-41:588:69//Hs.102761:U25029

45 F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318:73//Hs.159530:AC004957

50 F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635

F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911

55 F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353

EP 1 074 617 A2

F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220

5 F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56//Hs.143551:AF048693

10 F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575

F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:AF057280

15 F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs.155464:AF088219

20 F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs.17035:AI080471

F-HEMBA1005530

25 F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376

30 F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461

F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903

35 F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257

F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507

40 F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:AB007932

F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873

45 F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538

F-HEMBA1005582

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F-HEMBA1005583

55 F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381

F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA

EP 1 074 617 A2

FORMS//0.54:439:591/Hs.2137:D49357

5 F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323

F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609

10 F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982

F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:AF057280

15 F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//1.8e-89:454:96//Hs.19400:AA662845

20 F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535

F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734

25 F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199

F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956

30 F-HEMBA1005666

F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:AB011142

35 F-HEMBA1005679//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629

40 F-HEMBA1005680

F-HEMBA1005685

45 F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406

50 F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678

F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143

55 F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//2.6e-20:151:88//Hs.77393:D14697

F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754

EP 1 074 617 A2

- F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024
- 5 F-HEMBA1005755//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627
- F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219
- 10 F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141
- 15 F-HEMBA10058131//ESTs//0.012:209:63//Hs.113365:R77747
- F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346
- 20 F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577
- F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788
- 25 F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9e-42:690:66//Hs.23094:M19503
- 30 F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//Hs.79706:U53204
- F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150
- 35 F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.158095:AB007953
- 40 F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097
- F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.46468:U45984
- 45 F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766
- 50 F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081
- F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006
- 55 F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880

EP 1 074 617 A2

F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588

5 F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883

F-HEMBA1005963

10 F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516

F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530

15 F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526

F-HEMBA1006002

20 F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151

25 F-HEMBA1006031

F-HEMBA1006035

30 F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080

F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.41186:R99609

35 F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.43321:AI139422

F-HEMBA1006081

40 F-HEMBA1006090//EST//1.2e-12:340:62//Hs.61195:AI418788

F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313

45 F-HEMBA1006100//ESTs//7.1 e-22:273:73//Hs.144407:AA737799

F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741

50 F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968

55 F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222

F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:

EP 1 074 617 A2

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- 5 F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734
- F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881
- 10 F-HEMBA1006155
- F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575
- F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627
- 15 F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117
- F-HEMBA1006198//ESTs//0.017:133 :67//Hs.142168:AA292540
- 20 F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98//Hs.109268:AF070557
- 25 F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.7647:M94046
- F-HEMBA1006252
- 30 F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706
- F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158:69//Hs.159277:AB018341
- 35 F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631
- F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140
- 40 F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770
- F-HEMBA1006283
- 45 F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964
- F-HEMBA1006291
- 50 F-HEMBA1006293
- F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//Hs.46465:U45285
- 55 F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637:

EP 1 074 617 A2

68//Hs.37656:AB011174

- 5 F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350
- F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789
- 10 F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142
- F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220
- 15 F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287
- F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107:X59244
- 20 F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026
- F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422:59//Hs.80667:AF010233
- 25 F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922
- 30 F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531
- F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503
- 35 F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477
- F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881
- 40 F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830
- 45 F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835
- F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264
- 50 F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194
- F-HEMBA1006445
- 55 F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889
- F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124:AF019369

EP 1 074 617 A2

F-HEMBA1006467

5 F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:AI091453

F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257:AA875998

10 F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081

F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532

15 F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897

F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.28621:AA910431

20 F-HEMBA1006492

F-HEMBA1006494//ESTs//8.5e -24:299:72//Hs.153413:AI248625

25 F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389

F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072

30 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:AB014566

35 F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185

F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002

40 F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI160081

F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654:98//Hs.21301:AF093419

45 F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638

50 F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898

F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425

55 F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136

EP 1 074 617 A2

F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.44372:AI346522

F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479

5

F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778

10

F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219

15

F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB018295

F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862

20

F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875

F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:AI391502

25

F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI343331

F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589

30

F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185

35

F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:AA505003

40

F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196:U40282

F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615

45

F-HEMBA1006653

F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189

50

F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317

55

F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065

EP 1 074 617 A2

F-HEMBA1006676

5 F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575

F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145

10 F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198

F-HEMBA1006708

15 F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545

F-HEMBA1006717//ESTs//12.6e-31:286:78//Hs.55573:W37226

20 F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105

F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087

25 F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129727:AF035587

30 F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576:56//Hs.149323:AB002325

35 F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs.141073:W72720

F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657

40 F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250

F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798

45 F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503

50 F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298

F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III [C.elegans]//4.8e-110:523:98//Hs.125790:AA287723

55 F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:AI051551

F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624

EP 1 074 617 A2

F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970

5 F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327

F-HEMBA1006865

10 F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938

15 F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214

20 F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592

F-HEMBA1006914//EST//0.065 :366:6211Hs.162914:AA666199

25 F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989

F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154764:U16258

30 F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539

F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712

35 F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382

F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644:AJ010841

40 F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6940:Z48633

45 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740:94//Hs.14934:AF004828

F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase//1.9e-79:447:89//Hs.75268:X74570

50 F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968

55 F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723

F-HEMBA1007002

EP 1 074 617 A2

F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282

5 F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete
cds//2.5e-78:827:70//Hs.43003:AF035812

F-HEMBA1007045

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F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659

F-HEMBA1007052

15

F-HEMBA1007062

F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212

20

F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845

25 F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:
91//Hs.80510:M74002

F-HEMBA1007080

30

F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:
61//Hs.1974:M92432

35 F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA,
complete cds//0.95:541:57//Hs.3828:U49260

F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595

40

F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354

F-HEMBA1007121//ESTs//3.5e-69:335:98//Hs.140519:AA643182

45

F-HEMBA1007129

F-HEMBA1007147//ESTs//3.2e-07:235:641//Hs.124813:W46172

50

F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136

F-HEMBA1007151

55

F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318:
97//Hs.22396:AF062085

EP 1 074 617 A2

F-HEMBA1007178//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//4.2e-39:248:90//Hs.157148:AA311921

5 F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965

F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:
98//Hs.3363:D86987

10

F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252

15 F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6e-177:839:
98//Hs.27197:AB018340

F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
//2.7e-56:647:69//Hs.82314:M31642

20

F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:
U53204

25 F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:6411Hs.12432:
AF070575

F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//0.99:239:
60//Hs.111749:U13695

30

F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836

35 F-HEMBA1007279//ESTs//6. 1e-36:185:78//Hs.141022:H06475

F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529

40

F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637

F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062

45

F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74615

F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506

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F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634

F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241

55

F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens]//3.5e-09:
144:76//Hs.20597:W58370

EP 1 074 617 A2

F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130

5 F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006

F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561

10 F-HEMBB1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568

F-HEMBB1000008//H.sapiens mRNA for translin associated protein X//1.1e-43:370:78//Hs.96247:X95073

15 F-HEMBB1000018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs.83428:M58603

20 F-HEMBB1000024//EST//5.4e-07:137:70//Hs.125389:AA878307

F-HEMBB1000025//EST//0.99:362:58//Hs.121221:AA757392

25 F-HEMBB1000030//H.sapiens mRNA for cyclin II//1.3e-10:525:62//Hs.3232:Z46788

F-HEMBB1000036

30 F-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450:98//Hs.20815:AF084928

F-HEMBB1000039//EST//0.0034:97:73//Hs.141684:W35358

35 F-HEMBB1000044//ESTs//0.0048:218:63//Hs.123161:AA807319

F-HEMBB1000048//EST//0.00025:222:62//Hs.122474:AA765131

40 F-HEMBB1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717

F-HEMBB1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3e-54:259:88//Hs.23094:M19503

45 F-HEMBB1000055//ESTs//0.0017:289:62//Hs.125755:AA286923

50 F-HEMBB1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs.93121:AB018304

F-HEMBB1000083

55 F-HEMBB1000089//EST//0.0016:192:661//Hs.137093:AA917621

F-HEMBB1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645

EP 1 074 617 A2

5 F-HEMBB1000103//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:
74//Hs.103948:K00627

10 F-HEMBB1000113//EST//4.6e-23:221:76//Hs.142065:AA173763

15 F-HEMBB1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521

20 F-HEMBB1000136//ESTs112.3e-101:507:96//Hs.12659:AA195207

25 F-HEMBB1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044

30 F-HEMBB1000144//EST//4.5e-52:298:91//Hs.149580:AI281881

35 F-HEMBB1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:X92715

40 F-HEMBB1000175//EST//1.0:101:65//Hs.162898:AA659646

45 F-HEMBB1000198//EST//0.99:179:56//Hs.116880:AA662457

50 F-HEMBB1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4e-15:139:
82//Hs.101414:AB011129

55 F-HEMBB1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277

F-HEMBB1000218//EST//0.11:136:63//Hs.134683:AI092013

F-HEMBB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962

F-HEMBB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612

40 F-HEMBB1000244//ESTs//3.2e-15:139:81//HS.134549:AI078483

45 F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-
156:735:981//Hs.151411:AF075587

50 F-HEMBB1000258//EST//0.0091:325:60//Hs.97533:AA435884

55 F-HEMBB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4e-33:100:
100//Hs.27424:U75968

F-HEMBB1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)
//0.0019:373:60//Hs.16533:D87930

55 F-HEMBB1000272//ESTs//1.3e-93:440:99//Hs.I09224:N46684

EP 1 074 617 A2

F-HEMBB1000274//ESTs//0.41:221:65//Hs.71990:AA151796

5 F-HEMBB1000284//EST//0.00024:108:73//Hs.100725:F13689

F-HEMBB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574

10 F-HEMBB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.00092:252:65//Hs.41153:AB018326

F-HEMBB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787

15 F-HEMBB1000318//EST//0.014:184:61//Hs.155758:AI311870

F-HEMBB1000335//EST//0.99:187:63//Hs.137424:AA243729

20 F-HEMBB1000336//EST//1.0:209:63//Hs.150410:AI003611

F-HEMBB1000337//EST//0.086:133:66//Hs.128207:AA972330

25 F-HEMBB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127

F-HEMBB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:7611Hs.155464:AF088219

30 F-HEMBB1000341

F-HEMBB1000343//EST//0.66:163:63//Hs.150822:AI302729

35 F-HEMBB1000354//ESTs//7.e-61:292:100//Hs.152266:AA926874

40 F-HEMBB1000369//ESTs, Highly similar to t-BOP [M.musculus]/10.013:157:64//Hs.129982:AI420970

F-HEMBB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934

45 F-HEMBB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348

F-HEMBB1000391//ESTs//0.033:237:64//Hs.135289:AI092963

50 F-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4e-165:762:98//Hs.16184:AJ001642

55 F-HEMBB1000402//EST//0.013:291:59//Hs.149191:AI246155

F-HEMBB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194

EP 1 074 617 A2

F-HEM BB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925

5 F-HEM BB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete
cds//9.4e-73:364:83//Hs.129735AF010144

F-HEM BB1000438//ESTs//0.073:446:58//Hs.134632:AI223429

10 F-HEM BB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627

F-HEM BB1000449//EST//5.5e-21:356:671//Hs.157848:AI362501

15 F-HEM BB1000455//ESTs//0.092:147:65//Hs.106446:N93227

F-HEM BB1000472

20 F-HEM BB1000480//EST//0.98:83:71//Hs.146462:AI124898

F-HEM BB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206

25 F-HEM BB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560

F-HEM BB1000491

30 F-HEM BB1000493//ESTs//0.019:103:69//Hs.138358:T66178

35 F-HEM BB1000510//Glucocorticoid receptor alpha {alternative products}//1.6e-46:409:
77//Hs.102761:U25029

F-HEM BB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413

40 F-HEM BB1000523//ESTs//0.69:332:59//Hg.106845:W19543

F-HEM BB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-
terminus//2.1e-38:138:96//Hs.36131:Y11710

45 F-HEM BB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!!
[H.sapiens]//7.7e-31:554:67//Hs.157142:U85996

50 F-HEM BB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-
27:282:75//Hs.158095:AB007953

55 F-HEM BB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.0e-33:537:
65//Hs.5444:AB018293

F-HEM BB1000564

EP 1 074 617 A2

- F-HEMBB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001
- 5 F-HEMBB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238
- F-HEMBB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533
- 10 F-HEMBB1000589//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091
- 15 F-HEMBB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990
- F-HEMBB1000592//EST//0.0038:51:88//Hs.148022:AI269323
- 20 F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//Hs.3386:AF053356
- F-HEMBB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589
- 25 F-HEMBB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809
- F-HEMBB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864
- 30 F-HEMBB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI346481
- 35 F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349
- F-HEMBB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075
- 40 F-HEMBB1000638//EST//0.0076:92:75//Hs.125496:AA883735
- 45 F-HEMBB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830
- F-HEMBB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778
- 50 F-HEMBB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531
- 55 F-HEMBB1000665//EST//0.44:152:63//Hs.149534:AI280924
- F-HEMBB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2e-79:280:

EP 1 074 617 A2

85//Hs.23094:M19503

- 5 F-HEMBB1000673//ESTs//0.99:177:59//Hs.149864:N80474
- F-HEMBB1000684//Protein kinase, interferon-inducible double stranded RNA dependent//2.6e-31:220:87//Hs.73821:M35663
- 10 F-HEMBB1000693//Homo sapiens neuroanl mRNA, complete cds//5.3e-120:575:97//Hs.158300:AF040723
- 15 F-HEMBB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125
- F-HEMBB1000706//EST//8.6e-14:373:61//Hs.138281:RS5703
- F-HEMBB1000709//EST//0.99:110:651//Hs.162437:AA577510
- 20 F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56741
- F-HEMBB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216
- 25 F-HEMBB1000738//EST//5.9e-13:259:64//Hs.159699:AI417328
- F-HEMBB1000749//EST//3.1e-42:271:871//Hs.162197:AA535216
- 30 F-HEMBB1000763
- F-HEMBB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:72//Hs.38178:AA921830
- 35 F-HEMBB1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5 e-116:580:97//Hs.5009:AA081390
- 40 F-HEMBB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//Hs.86201:U78876
- 45 F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//3.0e-65:672:71//Hs.155983:AB014577
- 50 F-HEMBB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI133727
- F-HEMBB1000794//ESTs//0.00098:289:59//Hs.138782:N73572
- 55 F-HEMBB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI298375
- F-HEMBB1000810//ESTs//0.038:92:71//Hs.148763:AA66887

EP 1 074 617 A2

F-HEM BB1000821//EST//0.94:129:62//Hs.162299:AA555154

5 F-HEM BB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421

F-HEM BB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI283069

10 F-HEM BB1000827

F-HEM BB1000831

15 F-HEM BB1000835//EST//4.3e-27:201:851//Hs.141451:N29915

F-HEM BB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948

20 F-HEM BB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-135:875:85//Hs.23094:M19503

F-HEM BB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:61//Hs.311:U00238

25 F-HEM BB1000870//EST//0.00091:246:62//Hs.126502:AA913831

30 F-HEM BB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//Hs.128434:AF085351

F-HEM BB1000883//ESTs//0.42:107:67//Hs.154173:AI379823

35 F-HEM BB1000887

F-HEM BB1000888//ESTs//1.0:137:67//Hs.8121:AA521290

40 F-HEM BB1000890//ESTs//1.0:116:65//Hs.7105:T23433

F-HEM BB1000893//EST//0.0079:408:58//Hs.146504:AI129834

45 F-HEM BB1000908//EST//9.2e-21:205:79//Hs.132635:AI032875

50 F-HEM BB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//Hs.7938:D86984

F-HEM BB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049

55 F-HEM BB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI095468

F-HEM BB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089

EP 1 074 617 A2

F-HEM BB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593

F-HEM BB1000947

5

F-HEM BB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9.3e-48:572:72//Hs.2379:U23942

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F-HEM BB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938

F-HEM BB1000975//ESTs//0.78:180:66//Hs.104789:AA417124

15

F-HEM BB1000981

F-HEM BB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs.122967:AF059569

20

F-HEM BB1000991//EST//0.12:125:66//Hs.22945:R43713

F-HEM BB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055

25

F-HEM BB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193:62//Hs.119004:AB014565

30

F-HEM BB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025

F-HEM BB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384:67//Hs.108604:AC002310

35

F-HEM BB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991

40

F-HEM BB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247

F-HEM BB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61//Hs.129982:AI420970

45

F-HEM BB1001037//EST//0.0057:192:66//Hs.149987:AI291177

F-HEM BB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721

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F-HEM BB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687:X96586

55

F-HEM BB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149:96//Hs.15832:AB014518

F-HEM BB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs.155464:

EP 1 074 617 A2

AF088219

- 5 F-HEM BB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942
- F-HEM BB1001063
- 10 F-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736:95//Hs.12953:AF034803
- F-HEM BB1001096//EST//0.017:154:66//Hs.130403:AA909272
- 15 F-HEM BB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293
- F-HEM BB1001105//Human BRCA2 region, mRNA sequence
- 20 CG016//0.30:84:75//Hs.112434:U50529
- 25 F-HEM BB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:R06800
- F-HEM BB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062
- 30 F-HEM BB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139
- F-HEM BB1001119
- F-HEM BB1001126
- 35 F-HEM BB1001133//H.sapiens mRNA for translin associated protein X//1.2e-28:739:61//Hs.96247:X95073
- 40 F-HEM BB1001137
- F-HEM BB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:69//Hs.146395:AB002329
- 45 F-HEM BB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854
- F-HEM BB1001153//ESTs//7.6e-16:97:96//Hs.113307:H167.16
- 50 F-HEM BB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863
- 55 F-HEM BB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334
- F-HEM BB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS

EP 1 074 617 A2

CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183

5 F-HEMBB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129

F-HEMBB1001199

10

F-HEMBB1001208//ESTs//0.12:120:69//Hs.130093:AA928802

F-HEMBB1001209//EST//0.00028:215:65//Hs.118276:W15258

15

F-HEMBB1001210//EST//2.9e-05:297:60//Hs.88840:AA281452

20 F-HEMBB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157

F-HEMBB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.158241:AB007976

25

F-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]//6.7e-103:477:100//Hs.127835:AI378790

30 F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754

F-HEMBB1001249//EST//0.26:203:63//Hs.140791:AA935909

35

F-HEMBB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219

F-HEMBB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977

40

F-HEMBB1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//6.1e-24:146:78//Hs.51187:U82828

45 F-HEMBB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI359248

F-HEMBB1001282//GA-binding protein transcription factor, beta subunit 2 (47kD)//0.39:531:57//Hs.78915:U13045

50

* F-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.16606:W81021

55 F-HEMBB1001289//ESTs//6.4e-100:467:99//Hs.151720:AI287890

F-HEMBB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.3e-

EP 1 074 617 A2

135:654:98//Hs.124217:AA020848

F-HEMBB1001302

5

F-HEMBB1001304//ESTs//0.98:109:68//Hs.138972:AA047725

F-HEMBB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339

10

F-HEMBB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219

15

F-HEMBB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503

F-HEMBB1001326//ESTs//0.00030:257:63//Hs.62208:H12380

20

F-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:87//Hs.43071:AA206222

25

F-HEMBB1001335

F-HEMBB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:AB011135

30

F-HEMBB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694

35

F-HEMBB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878

F-HEMBB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142

40

F-HEMBB1001356//EST//0.32:292:59//Hs.135771:AI005648

F-HEMBB1001364

45

F-HEMBB1001366//EST//7.8e-24:367:69//Hs.138765:N70347

F-HEMBB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219

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F-HEMBB1001369//EST//0.17:211:63//Hs.120066:AA707973

55

F-HEMBB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:AB011099

EP 1 074 617 A2

F-HEMBB1001384

F-HEMBB1001387//ESTs//0.61:215:60//Hs.145915:AI342230

5

F-HEMBB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503

10

F-HEMBB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988

F-HEMBB1001424//EST//0.20:307:58//Hs.135336:AI049827

15

F-HEMBB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174

20

F-HEMBB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]//5.5e-153:729:96//Hs.21679:AF034175

25

F-HEMBB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345

F-HEMBB1001443

30

F-HEMBB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216

F-HEMBB1001454//ESTs//1.4e-46:279:93//Hs.104866:AA426038

35

F-HEMBB1001458//EST//1.7e-09:106:83//Hs.141422:N20920

40

F-HEMBB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220

45

F-HEMBB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740

F-HEMBB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:AB018303

50

F-HEMBB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088

F-HEMBB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942

55

F-HEMBB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815

EP 1 074 617 A2

- F-HEMBB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735
- 5 F-HEMBB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093
- F-HEMBB1001536//ESTs//0.0047:120:68//Hs.144858:R67748
- 10 F-HEMBB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306
- F-HEMBB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking
15 sequence//1.1e-35:188:77//Hs.102877:U41315
- F-HEMBB1001562//ESTs//0.95:161:61//Hs.145075:AI208240
- 20 F-HEMBB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953
- F-HEMBB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:
25 84//Hs.113283:AF018080
- F-HEMBB1001585
- 30 F-HEMBB1001586//EST//0.84:132:64//Hs.145264:AI218708
- F-HEMBB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:
35 U79289
- F-HEMBB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414
- F-HEMBB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680
- 40 F-HEMBB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314
- F-HEMBB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713
- 45 F-HEMBB1001635//ESTs//0.92:282:60//Hs.126980:AA934077
- F-HEMBB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:
50 AL009172
- F-HEMBB1001641//EST//0.11:53:81//Hs.112445:AA594279
- 55 F-HEMBB1001653//EST//0.91:124:64//Hs.144213:T40480
- F-HEMBB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:

EP 1 074 617 A2

473:63//Hs.54481:D86407

F-HEM BB1001668//ESTs//0.94:83:69//Hs.146202:AI252519

5

F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:AB014546

10

F-HEM BB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:100//Hs.106104:AA599496

F-HEM BB1001685//EST//2.2e-05:112:73//Hs.130984:AI015430

15

F-HEM BB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664

20

F-HEM BB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398

F-HEM BB1001706

25

F-HEM BB1001707//EST//0.091:241:60//Hs.136830:AA769219

F-HEM BB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064

30

F-HEM BB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219

35

F-HEM BB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485:97//Hs.120581:W25578

F-HEM BB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244

40

F-HEM BB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144

F-HEM BB1001753//ESTs//0.00013:35:100//Hs.139643:H06263

45

F-HEM BB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077

F-HEM BB1001760//ESTs//6.5e-06:503:58//Hs.21766:AI357639

50

F-HEM BB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.158241:AB007976

55

F-HEM BB1001785//EST//0.16:262:60//Hs.162526:AA584102

F-HEM BB1001797//ESTs//0.37:201:63//Hs.91559:AA806370

EP 1 074 617 A2

- F-HEMBB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951
- 5 F-HEMBB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.92381:AB007956
- F-HEMBB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017
- 10 F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//7.6e-164:763:98//Hs.159396:AF056209
- 15 F-HEMBB1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190
- F-HEMBB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067
- 20 F-HEMBB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370
- F-HEMBB1001850//EST//0.0035:204:61//Hs.7311:T23858
- 25 F-HEMBB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:82//Hs.155464:AF088219
- 30 F-HEMBB1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752
- F-HEMBB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371
- 35 F-HEMBB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503
- F-HEMBB1001872
- 40 F-HEMBB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923:Y12478
- F-HEMBB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein) //0.32:346:60//Hs.100555:X98743
- 45 F-HEMBB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868
- F-HEMBB1001899//ESTs//0.17:242:62//Hs.136969:AA830918
- 50 F-HEMBB1001905
- F-HEMBB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155
- 55 F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//1.2e-83:672:81//Hs.82210:U47742

EP 1 074 617 A2

F-HEMBB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62//Hs.159777:Z19955

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F-HEMBB1001911

F-HEMBB1001915//ESTs//0.92:136:71//Hs.144465:R68882

10

F-HEMBB1001921//EST//2.0e-19:398:67//Hs.44789:N36113

F-HEMBB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245

15

F-HEMBB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398

F-HEMBB1001930//EST//0.043:157:63//Hs.161927:AA483904

20

F-HEMBB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087

25

F-HEMBB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875

F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390

30

F-HEMBB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669

35

F-HEMBB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101

F-HEMBB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070

40

F-HEMBB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418

F-HEMBB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053

45

F-HEMBB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969

F-HEMBB1001973//Myelin oligodendrocyte glycoprotein {alternative products}//2.1e-48:426:78//Hs.53217:Z48051

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F-HEMBB1001983

55

F-HEMBB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051

F-HEMBB1001990//ESTs//0.25:171:64//Hs.7961:AA401205

EP 1 074 617 A2

F-HEMBB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103

5 F-HEMBB1001997//EST//5.3e-33:294:76//Hs.161041:H82636

F-HEMBB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964

10 F-HEMBB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093

F-HEMBB1002009//ESTs//0.066:441:58//Hs.125313:AI201685

15 F-HEMBB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951

F-HEMBB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699

20 F-HEMBB1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:217:60//Hs.3487:AA425553

F-HEMBB1002044

25 F-HEMBB1002045

F-HEMBB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256

30 F-HEMBB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661

35 F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:AB014512

F-HEMBB1002069

40 F-HEMBB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239

F-HEMBB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625

45 F-HEMBB1002115//EST//0.0083:244:64//Hs.125353:AA877080

F-HEMBB1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027

50 F-HEMBB1002139//ESTs//0.64:145:71//Hs.157821:AI362013

F-HEMBB1002142//ESTs//0.013:311:59//Hs.150037:AI292214

55 F-HEMBB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254

EP 1 074 617 A2

F-HEMBB1002189//EST//0.26:81:70//Hs.147726:AI220208

5 F-HEMBB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.16:608:58//Hs.4:
X03350

10 F-HEMBB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//Hs.301:
U18934

F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:405:
67//Hs.104115:X52332

15 F-HEMBB1002218//EST//0.015:241:61//Hs.105298:AA489813

F-HEMBB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:
AF088219

20 F-HEMBB1002247

F-HEMBB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B)
25 mRNA, complete cds//6.8e-47:418:77//Hs.125231:AF068006

F-HEMBB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:
77//Hs.154872:AB011166

30 F-HEMBB1002255//ESTs//0.017:255:61//Hs.126786:U74314

F-HEMBB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete
35 cds//0.17:511:57//Hs.58169:AF017790

F-HEMBB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998

40 F-HEMBB1002300

F-HEMBB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-
45 14:228:72//Hs.46468:U45984

F-HEMBB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083

50 F-HEMBB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:
96//Hs.105837:AA536054

F-HEMBB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188

55 F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:
98//Hs.42644:AJ010841

EP 1 074 617 A2

F-HEM BB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991

5 F-HEM BB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:U00943

F-HEM BB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838

10 F-HEM BB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796

F-HEM BB1002381

15 F-HEM BB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566

F-HEM BB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784

20 F-HEM BB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456

F-HEM BB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.0e-32:371:73//Hs.159897:AB007970

25

F-HEM BB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.54486:X54150

F-HEM BB1002442

30

F-HEM BB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:77//Hs.154326:D42087

35 F-HEM BB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101

F-HEM BB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274

40 F-HEM BB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-89:493:92//Hs.159605:U43885

45 F-HEM BB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds//0.019:228:63//Hs.74304:AF001691

F-HEM BB1002492//EST//0.24:149:62//Hs.146790:AI149051

50 F-HEM BB1002495//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//1.3e-22:331:71//Hs.30:M89796

55 F-HEM BB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494

F-HEM BB1002509//ESTs//0.017:220:63//Hs.155263:AI273725

EP 1 074 617 A2

F-HEM BB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354

5 F-HEM BB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-50:580:72//Hs.23094:M19503

F-HEM BB1002522//EST//0.010:172:62//Hs.147224:AI205719

10 F-HEM BB1002531

F-HEM BB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs.155464:AF088219

15

F-HEM BB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102

F-HEM BB1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648

20

F-HEM BB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191

F-HEM BB1002579//EST//1.0:77:68//Hs.147935:AI250286

25

F-HEM BB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095

F-HEM BB1002590//ESTs//0.64:132:63//Hs.155688:AI003657

30

F-HEM BB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336

F-HEM BB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-152:710:98//Hs.129826:AF089749

35

F-HEM BB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817

40

F-HEM BB1002603//EST//0.10:144:63//Hs.158180:AI367945

F-HEM BB1002607//ESTs//0.024:345:62//Hs.143304:AI084058

45

F-HEM BB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323

F-HEM BB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711

50

F-HEM BB1002614//ESTs//0.0048:136:71//Hs.106280:R13901

F-HEM BB1002617//EST//0.034:320:59//Hs.41223:H89127

55

F-HEM BB1002623//ESTs//0.88:222:60//Hs.129920:AA167217

F-HEM BB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs.151051:

EP 1 074 617 A2

U07620

- 5 F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811
- F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680
- 10 F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679
- F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124
- 15 F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674
- F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504
- 20 F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992
- F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614
- 25 F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588
- F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs.20814:AI242922
- 30 F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729
- F-MAMMA1000009//Human c-yes-1mRNA//1.0e-48:447:77//Hs.75680:M15990
- 35 F-MAMMA1000019
- F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750
- 40 F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945
- F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739
- 45 F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461
- 50 F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:AA001281
- 55 F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019
- F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840

EP 1 074 617 A2

F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067

5 F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:AB011174

10 F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//Hs.90357:U40705

F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792

15 F-MAMMA1000117

20 F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508

F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402

25 F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319

F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843

30 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585

35 F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924

F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050

40 F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695

F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530

45 F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657

50 F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739

55 F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035

F-MAMMA1000227//ESTs//0.010:268:60//Hs.16412:AA506926

EP 1 074 617 A2

F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913

5 F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873

F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587

10 F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543

F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015

15 F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874

F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087

20 F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726

25 F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361

F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505

30 F-MAMMA1000284

F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087

35 F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641

40 F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243

F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529

45 F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519

F-MAMMA1000313

50 F-MAMMA1000331

F-MAMMA1000339

55 F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:

EP 1 074 617 A2

AA180963

5 F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892

10 F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.158095:AB007953

F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503

15 F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087

20 F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569

F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344

25 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:98//Hs.32170:AB015132

30 F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590

F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503

35 F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:117:84//Hs.83916:U53468

40 F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725

F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092

45 F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111

F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532

50 F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:AF061573

55 F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459

F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641

EP 1 074 617 A2

F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:AF034546

5 F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830

10 F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:AB011166

F-MAMMA1000446

15 F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:93//Hs.9043:W21827

20 F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, complete cds//0.58:311:63//Hs.66721:D49818

25 F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830

F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

30 F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830

35 F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948

F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482

40 F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219

F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878

45 F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352

F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497

50 F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352

F-MAMMA1000565

55 F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//5.8e-51:404:80//Hs.125231:AF068006

EP 1 074 617 A2

- F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045
- 5 F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780
- F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//8.8e-45:390:78//Hs.159523:AF001622
- 10 F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744
- F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886
- 15 F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519
- 20 F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494
- F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478
- 25 F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605
- F-MAMMA1000623
- 30 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751
- 35 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474:AF023674
- F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353
- 40 F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4),3' end//9.0e-30:531:64//Hs.139107:K00629
- 45 F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490
- F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743
- 50 F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:U13220
- 55 F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627
- F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081

EP 1 074 617 A2

- 5 F-MAMMA1000713//Acetylcholinesterase {I4-E5 doman} [human, tumor cell lines, Genomic,
847 nt]//0.16:84:72//Hs.157124:S71129
- F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:6//Hs.27414:U79275
- 10 F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:
66//Hs.71148:AA854648
- F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247
- 15 F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:
72//Hs.114685:AA700024
- F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:
20 AF006513
- F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-
40:288:78//Hs.158095:AB007953
- 25 F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:
58//Hs.1742:L33075
- 30 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:
98//Hs.31575:AF100141
- F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580
- 35 F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:
88//Hs.153468:AB011147
- 40 F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494
- F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:
68//Hs.162011:AA513663
- 45 F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative products}//6.2e-47:341:
82//Hs.53217:Z48051
- 50 F-MAMMA1000761//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
[H.sapiens]//9.8e-19:131:76//Hs.118972:AA761369
- F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288
- 55 F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

EP 1 074 617 A2

F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114

F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137

5 F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575

10 F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849

F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130

15 F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089

F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e48:241:74//Hs.155464:AF088219

20 F-MAMMA1000841

F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//Hs.82210:U47742

25 F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696

30 F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877

F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022

35 F-MAMMA1000855

F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906

40 F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135

F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342

45 F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172

50 F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812

F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777

55 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459

EP 1 074 617 A2

F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147

5 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//1.4e-91:484:94//Hs.138938:AA012894

F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812

10 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465

F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:
211:63//Hs.76716:X67055

15 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683

F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506

20 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081

F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628

25 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239

F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429
30 nt]//1.0e-25:312:66//Hs.116007:S79267

F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968

35 F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of
branched chain keto acid dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785

F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734

40 F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:
63//Hs.83790:AB002303

45 F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:
64//Hs.25640:AB000714

50 F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474

F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete
cds//1.1e-56:310:85//Hs.129735:AF010144

55 F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814

F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096

EP 1 074 617 A2

F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802

5 F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062

F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007

10 F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724

F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711

15 F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:Y15718

F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968

20 F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds//3.6e-32:753:61//Hs.98384:AF062006

25 F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857

F-MAMMA1001038

30 F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178

F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI419882

35 F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719

40 F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503

F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585

45 F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116

F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749

50 F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503

55 F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420

F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896

EP 1 074 617 A2

- 5 F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254
- F-MAMMA1001092//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627
- 10 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045
- 15 F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915
- F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219
- 20 F-MAMMA1001133
- F-MAMMA1001139
- 25 F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534
- F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217
- 30 F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741
- F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147
- 35 F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299
- 40 F-MAMMA1001181
- F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171
- 45 F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083
- F-MAMMA1001198
- 50 F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348
- F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974
- 55 F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776

EP 1 074 617 A2

F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200

5 F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087

10 F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534

F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587

15 F-MAMMA1001244

F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476

20 F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121

F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149

25 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561

30 F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503

35 F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747

F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522

40 F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832

45 F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998

F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426

50 F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305

55 F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//1.9e-58:295:97//Hs.102336:Z83838

F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087

EP 1 074 617 A2

F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:
X57147

5 F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806

F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197

10 F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267

F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:
75//Hs.109358:AB018258

15 F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:273:
80//Hs.42674:U61981

20 F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID
LABILE CHAIN PRECURSOR//4.6e-09:415:58//Hs.839:M86826

25 F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:67//Hs.61333:
D83402

F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763

30 F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.0:176:
64//Hs.82001:U50928

35 F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80//Hs.43681:
AL022394

40 F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete
cds//0.00042:125:75//Hs.46328:D87942

F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:543:
71//Hs.37181:D64108

45 F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321

F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590

50 F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040

F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053

55 F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//2.0e-24:273:
72//Hs.75939:D78335

EP 1 074 617 A2

F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3.2e-25:397:68//Hs.116874:AA524909

5 F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366

F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0.99:258:61//Hs.154196:U87269

10

F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795

F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506

15

F-MAMMA1001547

F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5e-130:614:98//Hs.129937:AB007931

20

F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//0.71:181:62//Hs.118866:AI017072

25

F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M61764

F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339

30

F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132

F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375

35

F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23642:U79266

40

F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152

F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.158229:U28727

45

F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055//1.4e-40:447:73//Hs.154353:AL022165

50

F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:611:67//Hs.57679:U57796

55

EP 1 074 617 A2

F-MAMMA1001635

F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524

5

F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.00069:140:68//Hs.59829:AB014602

10

F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.015:135:71//Hs.27349:AB007917

15

F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819:AI027548

F-MAMMA1001671

20

F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317

F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889

25

F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765

F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549

30

F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, complete cds//8.0e-45:323:83//Hs.46468:U45984

35

F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548

F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926

40

F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.5e-111:725:84//Hs.159154:U47634

F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098

45

F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768

F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245

50

F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-67:822:69//Hs.23094:M19503

55

F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (HOHO1) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632

F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822

EP 1 074 617 A2

F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109

5 F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcript, partial//6.6e-41:309:84//Hs.102576:AJ010230

10 F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072

F-MAMMA1001768//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs.96028:AF042832

15 F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:686:79//Hs.113283:AF018080

20 F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//0.00071:392:60//Hs.32981:U38276

F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940

25 F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549

30 F-MAMMA1001788//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//6.7e-21:212:77//Hs.103948:K00627

F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72//Hs.5158:AB007869

35 F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987

F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884

40 F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:N47096

F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582

45 F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589

50 F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds//0.082:153:66//Hs.114948:AF059293

F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742

55 F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691

F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315, complete cds//2.0e-29:641:62//Hs.56808:D88827

EP 1 074 617 A2

F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665

5 F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028

F-MAMMA1001854

10 F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218

F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060

15 F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete
cds//0.084:672:58//Hs.152455:AF044209

F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687

20 F-MAMMA1001878

F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944

25 F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576

F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078

30 F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521

F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874

35 F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529

F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859

40 F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:
81//Hs.91916:AF035317

45 F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878

F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sapiens]//7.9e-09:150:
72//Hs.118222:N91115

50 F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633

F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826

55 F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915

EP 1 074 617 A2

F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159

5 F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.2e-54:455:70//Hs.158095:AB007953

F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580

10 F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225

F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256

15 F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305

F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-36:382:75//Hs.23094:M19503

20 F-MAMMA1002078

F-MAMMA1002082

25 F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012

F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//0.54:388:57//Hs.99423:AJ010840

30 F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120

35 F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932

F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs.155464:AF088219

40 F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:AI272963

F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:H52638

45 F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338

F-MAMMA1002145//EST//0.12:204:60//Hs.160983:AI392837

50 F-MAMMA1002153

F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335:97//Hs.88424:AA281385

55 F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)//0.99:310:

EP 1 074 617 A2

58//Hs.87149:M35999

F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196

5

F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X17206

F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:U39400

10

F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:121:98//Hs.146354:Z22548

15

F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362

F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120

20

F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645

F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:AI024063

25

F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//4.6e-69:344:90//Hs.76822:AI359536

30

F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//0.99:454:56//Hs.122755:AF032986

F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903

35

F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:AI308841

F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427:61//Hs.69949:M94172

40

F-MAMMA1002269

F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715

45

F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440

50

F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019

F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349:64//Hs.92614:M62302

55

F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460

EP 1 074 617 A2

- 5 F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57//Hs.77234:AB001914
- F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935
- 10 F-MAMMA1002308//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//6.9e-41:293:83//Hs.105292:AA504776
- F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA, complete
15 cds//0.0037:173:67//Hs.69423:AF055481
- F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-
41:473:65//Hs.92381:AB007956
- 20 F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291
- F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908
- 25 F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:
68//Hs.133342:AF070536
- F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515
- 30 F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPIP8) mRNA,
complete cds//0.0079:143:67//Hs.6755:AF055026
- 35 F-MAMMA1002332//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.2e-26:342:
72//Hs.103948:K00627
- 40 F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:
58//Hs.5333:AB018254
- F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6940:Z48633
- 45 F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//3.9e-14:146:81//Hs.163073:R02591
- F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907
- 50 F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:AI247086
- F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539
- 55 F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:
78//Hs.32511:AB007901

EP 1 074 617 A2

F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733

5 F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818

F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830

10 F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923

F-MAMMA1002362//EST//0.25:304:58//Hs.1.62427:AA576345

15 F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34677

F-MAMMA1002384//ESTs//1.1 e-05:220:65//Hs.141388:R52022

20 F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-118:578:97//Hs.25516:AI086362

F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624

25 F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632

F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737

30 F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745

F-MAMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788

35 F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030

F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087

40 F-MAMMA1002446

F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809

45 F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6.3e-06:595:59//Hs.99932:L38707

50 F-MAMMA1002470

F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.75074:U12779

55 F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059

EP 1 074 617 A2

- 5 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:
560:98//Hs.155223:AF055460
- F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628
- 10 F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:
63//Hs.133013:AA604920
- F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392
- 15 F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma)
mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214
- F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788
- 20 F-MAMMA1002554
- F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:
25 62//Hs.62354:M83822
- F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421
- 30 F-MAMMA1002571//EST//0.28:115:66//Hs.156768:AI351368
- F-MAMMA1002573//ESTs//2.1e-4.8:265:94//Hs.155128:AI224516
- 35 F-MAMMA1002585
- F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831
- 40 F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:AI334107
- F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958
- 45 F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220
- F-MAMMA1002612//ESTs, Moderately similar to hCDC10 protein [H.sapiens]//8.3e-18:353:
50 65//Hs.60895:AA428463
- F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357
- 55 F-MAMMA1002618
- F-MAMMA1002619

EP 1 074 617 A2

F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90//Hs.47344:AF041449

5 F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:N52300

F-MAMMA1002625

10 F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//1.1e-35:355:76//Hs.158241:AB007976

15 F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-05:439:61//Hs.91400:AB006626

F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733

20 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385

F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190

25 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:AI393335

F-MAMMA1002662//EST//0.99:95:63//Hs.144074:AI005489

30 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64//Hs.8262:U36336

35 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-06:272:64//Hs.106070:U22398

F-MAMMA1002673

40 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.2e-162:752:99//Hs.3363:D86987

45 F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:N69915

F-MAMMA1002698//ESTs//2.5e-09:190:68//Hs.138292:AI220397

50 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81//Hs.22396:AF062085

F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:AI274697

55 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.1e-51:307:79//Hs.46328:D87942

EP 1 074 617 A2

F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:N25041

5 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692

F-MAMMA1002727//EST//0.97:137:63//Hs.145153:AI150165

10 F-MAMMA1002728//ESTs, Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC
RIBONUCLEASE [*Saccharomyces cerevisiae*]//2.6e-12:129:81//Hs.154181:AA193502

F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853

15 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312

F-MAMMA1002748

20 F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848

F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98//Hs.32168:
AB007902

25 F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293

F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782

30 F-MAMMA1002769

F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein
35 (M8604 Met) gene//7.6e-84:417:97//Hs.77705:U07563

F-MAMMA1002780//EST//0.78:210:63//Hs.149413:AI273988

40 F-MAMMA1002782

F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:AI380710

45 F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919

F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:AI778514

50 F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-57:286:
88//Hs.15731:AB011135

55 F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:72//Hs.22271:
D26067

F-MAMMA1002835

EP 1 074 617 A2

- 5 F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN
1 [Locusta migratoria]//7.7e-38:179:78//Hs.141344:H29951
- F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590
- 10 F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4e-137:635:
99//Hs.7531:AB018353
- F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:329:
15 58//Hs.107747:AI357868
- F-MAMMA1002858
- F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643
- 20 F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696:78//Hs.83987:
U09284
- 25 F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423
- F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:AI183632
- 30 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//3.8e-30:
680:61//Hs.129732:D45027
- F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504:60//Hs.19944:
35 U04270
- F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657
- 40 F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666
- F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265
- 45 F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.00053:382:
57//Hs.61796:U85658
- F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952
- 50 F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125
- F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730
- 55 F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.9e-
103:485:99//Hs.102928:AI346344

EP 1 074 617 A2

- 5 F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.6e-194:910:98//Hs.31720:AB014598
- F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:AI423389
- 10 F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:AI313418
- F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:60//Hs.54697:AB007884
- 15 F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400
- F-MAMMA1002972
- 20 F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932
- F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944
- 25 F-MAMMA1002987//EST//0.044:254:59//Hs.135014:AI095645
- F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//3.9e-22:185:83//Hs.62192:J02931
- 30 F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.0e-16:343:61//Hs.159897:AB007970
- 35 F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979
- F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2e-51:620:69//Hs.75258:AF054174
- 40 F-MAMMA1003013//Human HOX4C mRNA for a homeobox protein//0.73:347:58//Hs.74061:X59372
- 45 F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062
- F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:AI374951
- 50 F-MAMMA1003026//EST//1.0:136:67//Hs.9123:T50137
- F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549
- 55 F-MAMMA1003035
- F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391

EP 1 074 617 A2

- 5 F-MAMMA1003040//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.5e-93:339:85//Hs.5247:AF029750
- F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D13639
- 10 F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans//1.0:209:60//Hs.99491:Y12336
- F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742
- 15 F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518
- F-MAMMA1003056
- 20 F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein MD6 [M.musculus]//1.3e-88:334:97//Hs.96500:AI206781
- F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:AI022618
- 25 F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5e-51:329:71//Hs.75154:AB014531
- 30 F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA, complete cds//8.5e-44:288:88//Hs.81008:AF043045
- 35 F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:213:60//Hs.42945:Y08136
- F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200:64//Hs.32950:X82634
- 40 F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, complete cds//5.4e-27:421:66//Hs.5394:AF105424
- 45 F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786
- F-MAMMA1003140
- 50 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//7.2e-82:397:97//Hs.151344:Y15062
- 55 F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.00019:297:61//Hs.108945:AB011087
- F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:487:65//Hs.3847:

EP 1 074 617 A2

U59632

5 F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//Hs.79706:
U53204

10 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:92//Hs.82510:
D31886

F-NT2RM1000032

15 F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:
81//Hs.78442:D83782

20 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5e-108:542:
95//Hs.60103:AB014590

F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//Hs.79706:
U53204

25 F-NT2RM1000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:353:
96//Hs.154980:AA948067

30 F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA,
complete cds//0.029:281:59//Hs.46465:U45285

F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210

35 F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:
97//Hs.3439:AC004472

40 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.8e-116:550:
97//Hs.65238:AB014561

45 F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190:63//Hs.431:
L13689

F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00086:126:
70//Hs.92693:AF007155

50 F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054

F-NT2RM1000127

55 F-NT2RM1000131

F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit

EP 1 074 617 A2

mRNA, nuclear gene encoding mitochondrial protein, complete cds//3.7e-92:448:97//Hs.49767:AF044959

5 F-NT2RM1000153//Homo sapiens mRNA for MTG8-related protein MTG16a, complete cds//1.0:546:58//Hs.110099:AB010419

10 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00081:126:70//Hs.92693:AF007155

F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:AI424382

15 F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.87:454:59//Hs.47061:AF045458

20 F-NT2RM1000242

F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.97:135:66//Hs.27910:AF049105

25 F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190

30 F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248:69//Hs.1674:M90516

F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H.sapiens]//2.9e-98:530:93//Hs.104650:AI037879

35 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:80//Hs.23106:D50920

40 F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047

F-NT2RM1000272

45 F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]//1.3e-21:308:73//Hs.15071:AA781144

F-NT2RM1000300

50 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708:92//Hs.5719:D63880

55 F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e-35:182:99//Hs.9837:D79205

F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976

EP 1 074 617 A2

- F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798
- 5 F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7e-75:387:95//Hs.108619:W28608
- F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691
- 10 F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.sapiens]//7.4e-91:481:95//Hs.163707:AA137181
- 15 F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X80507
- F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353
- 20 F-NT2RM1000399
- F-NT2RM1000421
- 25 F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.2e-85:418:97//Hs.20815:AF084928
- F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapiens]//1.6e-38:201:97//Hs.106262:AI052382
- 30 F-NT2RM1000539//EST//0.070:145:62//Hs.149711:AI284660
- 35 F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847
- F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:AI359957
- 40 F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:58//Hs.79706:U53204
- F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//0.98:226:61//Hs.17931:AB006625
- 45 F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]//6.2e-51:254:98//Hs.132096:AA314601
- 50 F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds//8.5e-55:276:97//Hs.19122:AF038957
- 55 F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60//Hs.113936:AB005297

EP 1 074 617 A2

F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:AI188279

F-NT2RM1000672

5

F-NT2RM1000691//Homo sapiens mRNA for HRIHFB2060, partial cds//7.0e-121:582:98//Hs.146282:AB015348

10

F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101

F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706

15

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//1.5e-66:435:85//Hs.5038:AJ004832

20

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.6e-127:690:92//Hs.147946:AB011139

25

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2e-68:524:83//Hs.112360:AF027208

F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465

30

F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:321:63//Hs.150390:AB007885

35

F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.053:271:60//Hs.139745 :U39067

F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frames//6.9e-20:128:94//Hs.23094:M19503

40

F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845

F-NT2RM1000800

45

F-NT2RM1000802

50

F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2e-64:490:84//Hs.112360:AF027208

F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:AI359957

55

F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//0.92:283:58//Hs.2314:X15422

F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:178:67//Hs.1376:

EP 1 074 617 A2

U26726

5 F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequence//3.8e-06:384:59//Hs.90314:L05148

10 F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//3.0e-149:726:97//Hs.99423:AJ010840

F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643

15 F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//5.3e-54:277:96//Hs.11125:AI015619

F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239

20 F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.0e-155:750:97//Hs.132898:AC004770

25 F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//8.8e-158:762:97//Hs.26285:AF082516

30 F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds//6.3e-19:310:67//Hs.65238:AB014561

F-NT2RM1000894

35 F-NT2RM1000898

F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:AI268701

F-NT2RM1000924//HOMEBOX PROTEIN HOX-A5//0.00051:458:59//Hs.37034:M26679

40 F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cds//0.084:386:58//Hs.101474:AB018350

45 F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:299:59//Hs.83419:D87440

50 F-NT2RM1000978

F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.3e-161:760:98//Hs.58488:U97067

55 F-NT2RM1001008//ESTs//1.3e-12:144:75//Hs.133122:AI025200

F-NT2RM1001043//EST//0.24:117:64//Hs.161536:N80395

EP 1 074 617 A2

- 5 F-NT2RM1001044//ESTs, Weakly similar to C43E11.9[C.elegans]//3.0e-98:491:96//Hs.102173:AA045270
- F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:533:57//Hs.79706:U53204
- 10 F-NT2RM1001066//ESTs//1.2e-114:538:99//Hs.129020:AI380703
- F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//0.69:586:56//Hs.62354:M83822
- 15 F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.0019:294:64//Hs.30223:X90846
- 20 F-NT2RM1001082//Archain//3.9e-37:290:81//Hs.33642:X81198
- F-NT2RM1001085
- 25 F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770:68//Hs.74107:X59244
- F-NT2RM1001102//ESTs//1.2e-35:638:63//Hs.131737:AI343331
- 30 F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246:63//Hs.75188:U10564
- F-NT2RM1001112//ESTs//8.9e-82:437:93//Hs.6330:H38495
- 35 F-NT2RM1001115
- F-NT2RM1001139//Keratin 9//1.5e-05:518:59//Hs.2783:Z29074
- 40 F-NT2RM2000006//ESTs//3.9e-16:96:98//Hs.101117:AA576113
- F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:640:59//Hs.148027:X63563
- 45 F-NT2RM2000030
- F-NT2RM2000032//ESTs//7.1 e-18:138:68//Hs.114031:AA700958
- 50 F-NT2RM2000042//ESTs//0.0091:241:61//Hs.147895:AI286243
- F-NT2RM2000092
- 55 F-NT2RM2000093//ESTs//2.6e-40:226:94//Hs.163521:H42085

EP 1 074 617 A2

F-NT2RM2000101//ESTs//1.0:235:61//Hs.48860:N27428

5 F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//5.8e-46:287:88//Hs.77271:X07767

10 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//3.0e-139:566:97//Hs.18953:AF067223

F-NT2RM2000192//EST//3.5e-07:168:65//Hs.163122:AA756999

15 F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans]//3.6e-93:489:95//Hs.143499:R72672

F-nnnnnnnnnnnn//ESTs//1.0e-70:269:97//Hs.156175:AI334328

20 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.0e-129:615:98//Hs.111862:AB011162

25 F-NT2RM2000259//ESTs//6.1e-30:172:85//Hs.116406:AA209520

F-NT2RM2000260//ESTs//2.5e-25:133:93//Hs.14169:AA203500

30 F-NT2RM2000287//ESTs//6.2e-13:97:83//Hs.118523:H98981

F-NT2RM2000322//Interferon regulatory factor 5//0.84:208:61//Hs.54434:U51127

35 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds//2.8e-176:805:99//Hs.129952:AB011132

F-NT2RM2000363//ESTs//1.2e-24:139:96//Hs.48818:N63543

40 F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds//3.7e-96:599:86//Hs.75871:U48251

45 F-NT2RM2000371

F-NT2RM2000374//ESTs//3.2e-13:98:91//Hs.65853:AI050866

50 F-NT2RM2000395//Growth arrest-specific 1//0.80:129:67//Hs.65029:L13698

F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714:59//Hs.28757:U81006

55 F-NT2RM2000407//ESTs//9.4e-92:458:96//Hs.148873:T33582

F-NT2RM2000420//EST//1.8e-61:296:99//Hs.147186:AI193053

EP 1 074 617 A2

F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4//1.5e-06:260:61//Hs.553:L05568

5 F-NT2RM2000452//ESTs//1.0:132:62//Hs.110004:AI097379

F-NT2RM2000469//ESTs//0.34:249:60//Hs.149575:AI281807

10 F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.4e-16:386:63//Hs.8309:AB018290

15 F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA, complete cds//0.99:272:61//Hs.76669:U08021

20 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//1.6e-172:824:97//Hs.4812:AF061243

F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.18:313:60//Hs.129725:AF047487

25 F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.7e-41:231:94//Hs.7049:AI141736

30 F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220

F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs.74369:AF032108

35 F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.89631:U48508

F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128

40 F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs.55609:W37993

45 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs.3363:D86987

F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220

50 F-NT2RM2000594

F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs.102402:AF040963

55

F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313

EP 1 074 617 A2

F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548

5 F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs.6150:AB011093

F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258

10 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs.19542:AB018272

15 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs.7278:AB014558

F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702

20 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs.115763:AB014576

25 F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:AI337371

F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs.5321:AF006083

30 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:64//Hs.7938:D86984

35 F-NT2RM2000718//Homa sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:594:98//Hs.136058:AB015342

F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107:X59244

40 F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464:91//Hs.161551:W24286

45 F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-82:640:81//Hs.5247:AF029750

50 F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//Hs.105919:AB002338

F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:AI346701

55 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2.8e-185:847:99//Hs.137580:AB015046

EP 1 074 617 A2

F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//6.2e-94:441:99//Hs.59075:AI023761

5 F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//Hs.84753:D87433

F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831

10

F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//2.9e-48:282:93//Hs.17035:AI080471

15 F-NT2RM2001065

F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:62//Hs.75111:D87258

20

F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.00079:274:59//Hs.102732:U88153

25 F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190

F-NT2RM2001141

30 F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042

F-NT2RM2001177

35 F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [C.elegans]//2.4e-23:149:93//Hs.10618:AI288739

F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959

40

F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630

45 F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349

F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766

50

F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U65928

55 F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:AF039694

EP 1 074 617 A2

F-NT2RM2001256

F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845

5

F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601

10

F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615

F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:AI138605

15

F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567

20

F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706

F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905

25

F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61//Hs.82925:U70322

F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382

30

F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378

F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:AJ007509

35

F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303

40

F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903

F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969

45

F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459

F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262

50

F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582:64//Hs.1042:M62800

55

F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077

EP 1 074 617 A2

F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902

5 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729

F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431

10

F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

15 F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918

F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:AB014518

20

F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952

25 F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92//Hs.22142:AA814725

F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

30

F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301

F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287

35

F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195

40 F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:671:97//Hs.27721:U17907

45 F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:AB011129

F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356

50

F-NT2RM2001675

F-NT2RM20016811//ESTs//0.16:197:63//Hs.20585:R10305

55

F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211

F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216

EP 1 074 617 A2

- 5 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937
- F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415
- 10 F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817
- F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826
- 15 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788
- F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650
- 20 F-NT2RM2001718
- F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123
- 25 F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:AB007931
- 30 F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:AB011132
- 35 F-NT2RM2001743
- F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399
- 40 F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
- F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:AI222742
- 45 F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669:71//Hs.2479:X78933
- F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698
- 50 F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:AI193595
- F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770
- 55 F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763

EP 1 074 617 A2

- 5 F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:U29175
- F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195
- 10 F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341
- F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068
- 15 F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691
- F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759
- 20 F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:86//Hs.113283:AF018080
- 25 F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567
- F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421:66//Hs.8763:W30741
- 30 F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723
- 35 F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198:AB014610
- F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892
- 40 F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937:AB007931
- 45 F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:U52840
- 50 F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U66688
- 55 F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//2.2e-139:653:98//Hs.21811:AF091080

EP 1 074 617 A2

F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392

F-NT2RM2001982

5

F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds//1.2e-21:123:98//Hs.6454:AF089816

10

F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.104135:AJ006778

15

F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538

F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:271:60//Hs.63888:AA203398

20

F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5e-37:509:65//Hs.6214:AB018274

25

F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:429:58//Hs.79090:D89729

30

F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822:73//Hs.1674:M90516

F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427

35

F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154

F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377

40

F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.89631:U48508

45

F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.5e-165:776:98//Hs.99423:AJ010840

F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435

50

F-NT2RM2002128

F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274

55

F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.4e-144:800:92//Hs.20815:AF084928

EP 1 074 617 A2

F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7e-165:787:97//Hs.11147:AB007936

5 F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)
//0.064:291:61//Hs.99936:X14487

10 F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59//Hs.148027:
X63563

F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074

15 F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464

F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674

20 F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI038511

F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product is related to human
RNA helicase A. [H.sapiens]//1.6e-30:369:70//Hs.114623:AI204280

25 F-NT2RM4000086

30 F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210)
mRNA, complete cds//1.3e-24:345:69//Hs.13128:AF060865

F-NT2RM4000139

35 F-NT2RM4000155

F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632

40 F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete
cds//9.8e-30:676:61//Hs.159228:AF041853

F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044

45 F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190

F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744

50 F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//0.13:322:61//Hs.145088:AI221147

55 F-NT2RM4000200

F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.0027:424:

EP 1 074 617 A2

60//Hs.91400:AB006626

5 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.4e-184:856:
98//Hs.111138:AB018255

10 F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013:358:
60//Hs.75055:M93651

F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.65:572:
60//Hs.47061:AF045458

15 F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582

F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439

20 F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccharomyces
pombe]//1.1e-16:112:92//Hs.93841:AA442297

25 F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete
cds//1.8e-48:229:83//Hs.46328:D87942

30 F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete
cds//2.5e-154:609:93//Hs.31305:M99438

F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds//0.070:
460:59//Hs.5372:AB000712

35 F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707

40 F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyces
cerevisiae]//2.7e-83:432:95//Hs.12796:W27884

F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:
68//Hs.155291:D13630

45 F-NT2RM4000354//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//0.0078:
55:92//Hs.59075:M023761

50 F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI418425

F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3e-135:628:
99//Hs.8152:AB014542

55 F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745

F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25.

EP 1 074 617 A2

Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:843:68//Hs.23796:AL022718

F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029

F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//4.9e-17:114:94//Hs.137580:AB015046

F-NT2RM4000421

F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432:74//Hs.154872:AB011166

F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543:58//Hs.2175:M59820

F-NT2RM4000457

F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178:631//Hs.66369:U95040

F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:AI280004

F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632

F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915

F-NT2RM4000514

F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409

F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:AI221305

F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756:96//Hs.125870:AI364967

F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:H78987

F-NT2RM4000534

F-NT2RM4000585

F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593:

EP 1 074 617 A2

62//Hs.7764:AB007938

5 F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]/3.1e-104:532:96//Hs.6092:T75227

10 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305:68//Hs.40100:AB002390

F-NT2RM4000611//EST//0.76:268:58//Hs.150031:AI292068

15 F-NT2RM4000616

F-NT2RM4000674

20 F-NT2RM4000689

F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529

25 F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744:77//Hs.42400:AF022789

30 F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]/2.6e-163:771:97//Hs.6823:W18181

35 F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:M84605

F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743:98//Hs.137168:AB018303

40 F-NT2RM4000741

45 F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]/1.1e-75:388:96//Hs.112361:R99396

F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:H67815

50 F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731

F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173:810:98//Hs.18586:AB007920

55 F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186

F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:

EP 1 074 617 A2

98//Hs.25817:AC005306

5 F-NT2RM4000795//ESTs, Highly Similar to LIVER CARBOXYLESTERASE PRECURSOR
[Homo sapiens]//6.7e-19:160:80//Hs.124902:AI337820

10 F-NT2RM4000796//Human K+ channel subunit gene, complete cds//0.96:292:
62//Hs.124212:M64676

F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301

15 F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subunit
(SNAP190) mRNA, complete cds//0.052:238:64//Hs.113265:AF032387

F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H16568

20 F-NT2RM4000833

F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374:61//Hs.7841:
25 AB002322

F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934

30 F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN
SUBSTRATE 2 [Homo sapiens]//4.4e-29:164:95//Hs.115095:AI392943

F-NT2RM4000887

35 F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine
pyrophosphorylase, complete cds//6.8e-22:407:64//Hs.21293:AB011004

40 F-NT2RM4000950

F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546

45 F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:
77//Hs.7289:AB007875

F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381:67//Hs.2481:X78926

50 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6e-171:803:
98//Hs.19542:AB018272

55 F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1e-126:584:
99//Hs.15711:AB014539

F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.8e-05:469:

EP 1 074 617 A2

58//Hs.5333:AB018254

5 F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus]//7.0e-56:340:
92//Hs.87310:AI247543

10 F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM"
PRECURSOR//0.79:142:69//Hs.77424:M63835

F-NT2RM4001084

15 F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:
62//Hs.108947:D30758

F-NT2RM4001116

20 F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:
61//Hs.134989:L12701

25 F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730

F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:AI004145

30 F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351

F-NT2RM4001187

35 F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220

F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799:69//Hs.2479:X78933

40 F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.4e-
153:707:99//Hs.14934:AF004828

45 F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1
IN CHROMOSOME III [Caenorhabditis elegans]//0.19:291:62//Hs.31582:AA877205

F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete
cds//7.0e-63:715:70//Hs.104925:AF059611

50 F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog
[C.elegans]//1.1e-67:208:96//Hs.26676:AA033997

55 F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.0019:435:
59//Hs.6360:AB007950

F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:

EP 1 074 617 A2

59//Hs.26971:AC003003

5 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973

F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335

10 F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:66//Hs.87435:D89016

F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AI418988

15 F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0096:284:58//Hs.120997:R56714

20 F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.7e-52:252:100//Hs.15301:AA167818

25 F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI277656

F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790:98//Hs.5151:AF098799

30 F-NT2RM4001384

35 F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575

F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64//Hs.105052:AB000520

40 F-NT2RM4001412

45 F-NT2RM4001414//ESTs, Moderately similar to 18547_1 [H.sapiens]//5.2e-18:133:87//Hs.28209:AI073817

F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:70//Hs.154326:D42087

50 F-NT2RM4001444

F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658

55 F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914

F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36

EP 1 074 617 A2

[H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784

5 F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:AB014585

F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619

10 F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae]//1.3e-114:536:99//Hs.88820:AA456247

F-NT2RM4001557

15

F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487

20 F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453

F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859

25

F-NT2RM4001582

F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566

30 F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:AB011094

35 F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077

F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:AB018334

40

F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739

45 F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens]//0.0042:153:68//Hs.114832:AI147946

50 F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320

55

F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323

EP 1 074 617 A2

F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638

F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384

5

F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957

10

F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905

F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903

15

F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318

20

F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306

25

F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719

F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:X97630

30

F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:AB018270

35

F-NT2RM4001783//ESTs, Weakly similar to T12D8.i [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677

40

F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105

F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547

45

F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712

50

F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:AI379442

F-NT2RM4001828//Zinc fmger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687

55

F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953 :M96824

F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204

EP 1 074 617 A2

- F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814
- 5 F-NT2RM4001856
- F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250
- 10 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.3e-150:704:98//Hs.61628:Y17711
- 15 F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984
- F-NT2RM4001880
- 20 F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212
- F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:AI312633
- 25 F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356:AJ224875
- 30 F-NT2RM4001938
- F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:AF098162
- 35 F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087
- 40 F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//1.8e-65:337:96//Hs.130135:AA905493
- F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862
- 45 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:AB018341
- 50 F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082
- F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936
- 55 F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271

EP 1 074 617 A2

F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601

F-NT2RM4002034

5

F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048

F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912

10

F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540

15

F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//7.0e-94:396:94//Hs.59346:AI126802

F-NT2RM4002063

20

F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309

25

F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040

F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302

30

F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.122967:AF059569

35

F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//9.2e-34:532:65//Hs.146459:X66975

F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743

40

F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542

45

F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877

50

F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158

F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens]//1.6e-135:646:97//Hs.104650:AI037879

55

F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:

EP 1 074 617 A2

95//Hs.22464:AF084535

F-NT2RM4002174

5

F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998

10

F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:U38276

F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454

15

F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182

20

F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//8.4e-125:588:98//Hs.23900:U82984

F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966

25

F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764

30

F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118

F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180

F-NT2RM4002281

35

F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979

40

F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457

F-NT2RM4002301

45

F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331

F-NT2RM4002339

50

F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454

55

F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708:98//Hs.26163:AB014549

F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303:63//Hs.23741:AB018263

EP 1 074 617 A2

- F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293
- 5 F-NT2RM4002390
- F-NT2RM4002398
- 10 F-NT2RM4002409
- F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog
[C.elegans]//1.1e-55:282:96//Hs.26676:AA033997
- 15 F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:
AF052151
- 20 F-NT2RM4002452
- F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:
81//Hs.115263:D30783
- 25 F-NT2RM4002460//EST//1.0:142:65//Hs.145370:AI252780
- F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-
165:777:98//Hs.8765:AF083255
- 30 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:
97//Hs.94781:AB014591
- 35 F-NT2RM4002493
- F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347
- 40 F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:
AF088219
- 45 F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:
290:60//Hs.154968:U02020
- 50 F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:
D87075
- F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor All/AVP mRNA,
complete cds//1.0:100:70//Hs.159483:AF054176
- 55 F-NT2RM4002558//Homo sapiens amphiphysin II mRNA, complete cds//0.17:393:
61//Hs.6619:U84004

EP 1 074 617 A2

- 5 F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:D84273
- F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans]//3.3e-88:484:93//Hs.105837:AA536054
- 10 F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase [H.sapiens]//0.059:121:70//Hs.155413:AA429394
- F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151
- 15 F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499:59//Hs.79357:D78275
- 20 F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402
- F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587
- 25 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:AJ012449
- 30 F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907
- F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647
- 35 F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834
- F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792:AF044924
- 40 F-NT2RP1000111
- 45 F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699
- F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:AI084025
- 50 F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:382:94//Hs.127842:W38901
- 55 F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90//Hs.3760:AF011792
- F-NT2RP1000170//EST//0.68:130:63//Hs.146994:AI184430

EP 1 074 617 A2

- 5 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:
97//Hs.78019:AF070535
- F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499
- 10 F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:
58//Hs.74019:X83703
- F-NT2RP1000243
- 15 F-NT2RP1000259
- F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete
cds//5.4e-109:528:97//Hs.4214:AF067730
- 20 F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661
- F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding
25 mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551
- F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-
10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231
- 30 F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:
U53204
- 35 F-NT2RP1000357
- F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807
- 40 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:
86//Hs.77864:AB014538
- F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete
45 cds//5.9e-178:877:96//Hs.120360:AF064594
- F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031
- 50 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:
98//Hs.21862:AB011159
- 55 F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1
PRECURSOR [Mus musculus]//7.3e-177:857:97//Hs.6823:W18181
- F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA,

EP 1 074 617 A2

complete cds//0.46:222:60//Hs.89230:AF031815

F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603

5

F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862

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F-NT2RP1000460

F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence//3.7e-134:665:96//Hs.143187:AC002985

15

F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs.159154:U47634

20

F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102

F-NT2RP1000493

25

F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977

F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992

30

F-NT2RP1000547//H.sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098

35

F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.104105:AF017418

40

F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213

45

F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385

F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770

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F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.152936:D63475

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F-NT2RP1000630

F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:U24576

EP 1 074 617 A2

- 5 F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553
- F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:AI141736
- 10 F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148
- F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D30612
- 15 F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens]//6.2e-40:297:84//Hs.18122:AI338045
- 20 F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644
- F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434
- 25 F-NT2RP1000746
- F-NT2RP1000767
- 30 F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023
- F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401
- 35 F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//2.7e-23:147:91//Hs.102336:Z83838
- 40 F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424:96//Hs.18953:AF0672 23
- 45 F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332903
- F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI267990
- 50 F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI288838
- F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875
- 55 F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023
- F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:

EP 1 074 617 A2

95//Hs.125156:AF064094

F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218683

5

F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:AI248847

F-NT2RP1000916//ESTs, Weakly similar to coded for by C. elegans cDNA cm04e9
[C.elegans]//2.2e-27:159:94//Hs.122153:AA780270

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F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248

15

F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400

F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA,
complete cds//2.7e-26:185:87//Hs.108332:U39317

20

F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:
AB002803

25

F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847

F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M17885

30

F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858

F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866

35

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:
L13435

F-NT2RP1001011

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F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163

F-NT2RP1001014

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F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764

F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901

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F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531

F-NT2RP1001080//Homo sapiens forkhead protein (FKHRL1) mRNA, complete cds//0.57:
215:64//Hs.14845:AF032886

55

F-NT2RP1001113//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F

EP 1 074 617 A2

[C.elegans]//1.4e-65:293:95//Hs.32751:H38087

F-NT2RP1001173

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F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258:AF054174

10

F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524

F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150

15

F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.25195:U81523

F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094

20

F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:AJ002231

25

F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724

F-NT2RP1001294

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F-NT2RP1001302

35

F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341

F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815

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F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770

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F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]//6.8e-101:480:94//Hs.75017:AA166853

F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859

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F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673

F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081

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F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700

EP 1 074 617 A2

F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700

5 F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:
AF052149

F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104

10 F-NT2RP1001466

F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742

15 F-NT2RP1001482

F-NT2RP1001494

20 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400

F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:
25 64//Hs.75814:AB000277

F-NT2RP1001569

30 F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds//2.5e-41:496:
74//Hs.12956:U90913

F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420

35 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//4.7e-
137:685:96//Hs.93677:AF091081

40 F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C .elegans]//8.2e-47:300:89//Hs.6473:
AA853955

F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:
45 AB002390

F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:
D31763

50 F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
[Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359

55 F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:
97//Hs.8309:AB018290

EP 1 074 617 A2

- 5 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749
- 10 F-NT2RP2000054//HOMEBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433
- 15 F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.155991:X54134
- 20 F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022718 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609
- F-NT2RP2000076//H.sapiens mRNA for TFIIA//0.00023:356:62//Hs.121686:D14887
- 25 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078
- 30 F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879
- F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338
- 35 F-NT2RP2000091
- F-NT2RP2000097
- 40 F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963
- F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390
- 45 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706:AB018356
- 50 F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670
- 55 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177
- F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195

EP 1 074 617 A2

- 5 F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.152936:D63475
- F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910
- 10 F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291
- F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190
- 15 F-NT2RP2000173
- F-NT2RP2000175
- 20 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//Hs.100058:AB006713
- 25 F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:AI148761
- F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050
- 30 F-NT2RP2000208
- F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:243:61//Hs.143641:AB009462
- 35 F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990
- 40 F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342:59//Hs.8546:U97669
- F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//Hs.47822:AB002378
- 45 F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719
- 50 F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.51:227:60//Hs.30223:X90846
- F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691
- 55 F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011
- F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599

EP 1 074 617 A2

- F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910
- 5 F-NT2RP2000288
- F-NT2RP2000289
- 10 F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744:70//Hs.37138:U35376
- F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:AI123467
- 15 F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//4.3e-13:140:80//Hs.58218:U82381
- 20 F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:AI417006
- F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:AI332905
- 25 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66//Hs.101642:X60673
- F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:126:69//Hs.153706:AF026547
- 30 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.2e-130:627:97//Hs.76556:U83981
- 35 F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.56:464:57//Hs.12259:AB014530
- 40 F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047
- F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67:375:93//Hs.808:L28010
- 45 F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapiens]//3.9e-75:413:92//Hs.36779:AA626790
- 50 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//6.7e-128:609:96//Hs.5819:AF102265
- F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381
- 55 F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402:AI393918

EP 1 074 617 A2

F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e-22:158:87//Hs.154655:Z68747

F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293

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F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702

F-NT2RP2000510

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F-NT2RP2000516

F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B MRNA EDITING PROTEIN
[Rattus norvegicus]//3.2e-15:167:75//Hs.10984:AA806768

15

F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6e-38:196:
98//Hs.14409:AB011144

20

F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy,
hypertrophic 1)//1.0:242:57//Hs.114001:Z20656

25

F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732:
97//Hs.7314:AB014514

F-NT2RP2000644//ESTs//0.035:276:60//Hs.43660:N33174

30

F-NT2RP2000656

F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602

35

F-NT2RP2000668

F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:AI093453

40

F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN
KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233:
78//Hs.114905:AA088442

45

F-NT2RP2000710

F-NT2RP2000715

50

F-NT2RP2000731

F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA573242

55

F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces
cerevisiae]//1.6e-74:445:89//Hs.21421:AA911739

EP 1 074 617 A2

F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101

5 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:58//Hs.159275:AF030880

F-NT2RP2000814

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F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182

15 F-NT2RP2000819

F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:70//Hs.20695:AB002292

20

F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//9.5e-29:167:94//Hs.75794:U80811

25 F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:AI336850

F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]//6.4e-34:207:92//Hs.135235:AI081880

30

F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732:94//Hs.3615:AB018284

35 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.50:189:65//Hs.46146:AA418097

F-NT2RP2000931//MATRIN3//1.1e-130:610:98//Hs.78825:AB018266

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F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326:97//Hs.15144:AC005014

45 F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408

F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533:98//Hs.19822:AB018298

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F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494

F-NT2RP2000970

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F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [Saccharomyces cerevisiae]//7.3e-76:385:96//Hs.21875:

EP 1 074 617 A2

AA243700

- 5 F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944
- F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292
- 10 F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117
- F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696:97//Hs.67619:AB007957
- 15 F-NT2RP2001065
- F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313
- 20 F-NT2RP2001081
- F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:AI356560
- 25 F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219
- 30 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:63//Hs.80358:U52191
- 35 F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34:201:91//Hs.118470:AI336362
- F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582
- 40 F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:AI091361
- F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567:96//Hs.26247:AB007949
- 45 F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011
- F-NT2RP2001196
- 50 F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598
- F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053
- 55 F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//Hs.69740:U09367

EP 1 074 617 A2

- F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813
- 5 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353
- F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277
- 10 F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:76//Hs.75848:U39412
- 15 F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287
- F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387
- 20 F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs.76090:M80783
- F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522
- 25 F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41883
- F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418:91//Hs.107039:W27244
- 30 F-NT2RP2001378
- 35 F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:AI377558
- F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//0.28:225:62//Hs.159402:AC005609
- 40 F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767
- F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088
- 45 F-NT2RP2001420
- F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]//0.030:443:59//Hs.140506:AA308018
- 50 F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875
- 55 F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966
- F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation

EP 1 074 617 A2

protein, eta polypeptide//9.8e-56:603:72//Hs.75544:Z82248

F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218

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F-NT2RP2001449

F-NT2RP2001450

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F-NT2RP2001467

F-NT2RP2001506

15

F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409:98//Hs.156161:AI333779

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F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.4e-138:657:97//Hs.4277:Y14494

F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134

25

F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//5.2e-105:384:94//Hs.99742:AF035586

30

F-NT2RP2001560

F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs.67619:AB007957

35

F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389

40

F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876

F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//Hs.82201:M55268

45

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:AB018340

50

F-NT2RP2001613

F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI082229

55

F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96//Hs.58488:U97067

EP 1 074 617 A2

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds//1.3e-145:687:97//Hs.159558:AF058718

5 F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328

F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58//Hs.96264:U72936

10 F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314

15 F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621 :U52840

F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091

20 F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:AI197870

25 F-NT2RP2001721

F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991

30 F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//1.2e-19:151:86//Hs.77393:D14697

35 F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete_cds//5.2e-34:191:96//Hs.47504:AF091754

F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180

40 F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI052250

F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610

45 F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443:AF027219

50 F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768

F-NT2RP2001883

55 F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR//3.0e-113:633:90//Hs.142189:M74161

F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650

EP 1 074 617 A2

- 5 F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]/0.37:263:62//Hs.106377:H29757
- F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI393754
- F-NT2RP2001936
- 10 F-NT2RP2001943
- F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797
- 15 F-NT2RP2001947
- F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489
- 20 F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892
- 25 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:AB011117
- F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196
- 30 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:AB018299
- 35 F-NT2RP2002032
- F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI003543
- 40 F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336
- F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678 :R51509
- 45 F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284198
- F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284
- 50 F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:66//Hs.44553:AF055634
- 55 F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241
- F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:

EP 1 074 617 A2

96//Hs.11039:AF052183

F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014

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F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI313156

F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533:
97//Hs.155218:AJ007509

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F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete
cds//6.1e-07:408:60//Hs.122755:AF032986

15

F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286

F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:
59//Hs.995:M83363

20

F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:
AJ008112

25

F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314

F-NT2RP2002185//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//6.8e-61:354:
91//Hs.109966:C06057

30

F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7e-37:194:
97//Hs.91728:M58460

35

F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha
mRNA, complete cds//6.8e-15:228:67//Hs.111323:AF077954

40

F-NT2RP2002208

F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628

45

F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394318

F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264:U70439

50

F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.79:264:
59//Hs.129748:AB011099

F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//2.1e-51:
315:89//Hs.150595:AF005418

55

F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//Hs.92137:

EP 1 074 617 A2

M19720

5 F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]/1.3e-31:206:88//Hs.4029:Z78373

F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079

10 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//5.0e-95:467:96//Hs.24812:AF069532

15 F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445

F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.3e-124:640:95//Hs.31034:AB015594

20 F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60//Hs.75516:X54637

F-NT2RP2002373

25 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.1e-139:673:97//Hs.109051:AF038958

30 F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U79289

F-NT2RP2002408//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74095:L20433

35 F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098

F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326

40 F-NT2RP2002442//ESTs, Weakly similar to similar to molybdoterin biosynthesis MOEB proteins [C.elegans]/5.6e-26:169:89//Hs.25198:AA904265

45 F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs.1560:D42045

50 F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:AI139929

F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs.125856:AB005289

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F-NT2RP2002498

EP 1 074 617 A2

F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs.102681:U95044

5 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs.23255:AB018334

10 F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563:M28212

F-NT2RP2002537

15 F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096

F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979

20 F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs.159277:AB018341

F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309

25 F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs.23094:M19503

30 F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs.334:U02082

35 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805

F-NT2RP2002621

40 F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs.155302:U57317

F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493

45 F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109857:AA088385

50 F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs.6336:AB014572

55 F-NT2RP2002727

F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217

EP 1 074 617 A2

F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297

5 F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs.87435:D89016

10 F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs.146395:AB002329

F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709

15 F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705

F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs.79706:U53204

20 F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407

F-NT2RP2002800

25 F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763

F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:AI382142

30 F-NT2RP2002862

F-NT2RP2002880

35 F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0:237:62//Hs.106487:AB014573

40 F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606

F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.116674:AF038392

45 F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:158:65//Hs.108447:AJ000517

50 F-NT2RP2002939

F-NT2RP2002954

55 F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds//6.4e-21:135:91//Hs.108332:U39317

EP 1 074 617 A2

F-NT2RP2002979

F-NT2RP2002980

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F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs.122967:AF059569

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F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:AI004740

F-NT2RP2002993

15

F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs.155464:AF088219

20

F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741

F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019

25

F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190

F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs.153704:U11050

30

F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633

35

F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:AI291379

F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:556:57//Hs.155321:J03161

40

F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544

F-NT2RP2003137

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F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227:61//Hs.105958:AB014520

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F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581:93//Hs.9736:D67025

F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:AI424170

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F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944

F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:

EP 1 074 617 A2

79//Hs.153014:AB002353

F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:N91123

5

F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:AI393223

F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594

10

F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794

F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947

15

F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//Hs.108966:U48696

20

F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:200:62//Hs.102732:U88153

F-NT2RP2003265

25

F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//5.8e-57:313:93//Hs.109966:C06057

30

F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714:96//Hs.154919:AB014525

F-NT2RP2003280

35

F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243:65//Hs.21862:AB011159

40

F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:AI269334

F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds//2.0e-86:416:97//Hs.7943:AB006572

45

F-NT2RP2003297//EST//0.99:240:60//Hs.133228:AI052312

F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752

50

F-NT2RP2003308

F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:532:95//Hs.6092:T75227

55

F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:AI346765

EP 1 074 617 A2

F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963

5 F-NT2RP2003367//Human HsLIM15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108

F-NT2RP2003391

10

F-NT2RP2003393

15 F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023

F-NT2RP2003401

20 F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//3.7e-33:303:77//Hs.14038:R06800

F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893

25

F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273:61//Hs.159360:L22647

F-NT2RP2003456//EST//0.17:95:65//Hs.147190:AI193320

30

F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770

35 F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106

F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136

40

F-NT2RP2003506

F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.107164:M96803

45

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:94//Hs.78482:Y16270

50 F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783

F-NT2RP2003522//Zinc finger protein 148 (pHZ-52)//1.1e-17:512:60//Hs.112180:AF039019

55

F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765

EP 1 074 617 A2

F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010

F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:AI356513

5

F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800

10

F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937:AB007931

F-NT2RP2003581//EST//1.0:59:76//Hs.158575:AI368947

15

F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//1.3e-63:224:95//Hs.34627:AA126463

20

F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98//Hs.58488:U97067

F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166

25

F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252

30

F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006

F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:AI032875

35

F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247

F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561

40

F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44:269:91//Hs.139757:N95271

45

F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097

F-NT2RP2003713

50

F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180

55

F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879

F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme Ubch5C (UBCH5C) mRNA,

EP 1 074 617 A2

complete cds//4.0e-55:584:71//Hs.118797:U39318

5 F-NT2RP2003751

F-NT2RP2003760

10 F-NT2RP2003764

F-NT2RP2003769

15 F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677

F-NT2RP2003777

20 F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63:356:92//Hs.16131:AA568689

25 F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955

F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742

30 F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368

F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425

35 F-NT2RP2003859

F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780

40 F-NT2RP2003885

F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emericella nidulans]//2.2e-113:632:92//Hs.50072:AI378221

45 F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]//1.0:146:67//Hs.156920:AA489296

50 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs.35086:AB014458

55 F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:AB007916

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347

EP 1 074 617 A2

- F-NT2RP2003984
- 5 F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036
- F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369
- 10 F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//7.0e-104:556:93//Hs.111081:AI380378
- F-NT2RP2004014
- 15 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780
- 20 F-NT2RP2004042
- F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:AF011573
- 25 F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942
- F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199:60//Hs.104315:AF054828
- 30 F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292
- 35 F-NT2RP2004142
- F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872
- 40 F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666
- F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966
- 45 F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501
- F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.7e-16:276:67//Hs.36779:AA626790
- 50 F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:U57317
- 55 F-NT2RP2004196

EP 1 074 617 A2

F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756

5 F-NT2RP2004226//ESTs, Weakly Similar to teg292 protein [M.musculus]//1.8e-80:386:98//Hs.68791:AA527270

F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756

10 F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680

F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536

15 F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487

20 F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans]//8.2e-51:474:74//Hs.108990:N25951

F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//Hs.12432:AC005263

25

F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:157:67//Hs.37121:Z37544

30 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:AF000416

35 F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735

F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510

40 F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632

F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202

45 F-NT2RP2004365

F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs.39163:AF000986

50 F-NT2RP2004373

55 F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.3e-97:477:98//Hs.30490:AA146916

F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588

EP 1 074 617 A2

F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21//1.4e-174:875:95//Hs.152759:AC005164

5 F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans]//1.2e-92:519:91//Hs.13275:AI341468

10 F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367

F-NT2RP2004412

15 F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944

F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687

20 F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TASK) mRNA, complete cds//0.45:208:61//Hs.24040:AF006823

F-NT2RP2004490

25 F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203

30 F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.3e-29:270:79//Hs.73614:U83460

F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6e-139:687:96//Hs.129908:AB011163

35 F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891

40 F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-06:291:61//Hs.132206:AF039694

F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs.155464:AF088219

45 F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.98:136:64//Hs.28020:AB018309

50 F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.0:104:68//Hs.125729:N99898

55 F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.24756:U43895

F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-59:273:93//Hs.12845:N28835

EP 1 074 617 A2

- F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908
- 5 F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496:98//Hs.5198:AJ006291
- 10 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2e-155:728:98//Hs.29956:AB007929
- F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839
- 15 F-NT2RP2004681
- F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327:94//Hs.154919:AB014525
- 20 F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942
- F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780
- 25 F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582:96//Hs.4236:AB007947
- 30 F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242
- F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183
- 35 F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]//3.7e-110:548:96//Hs.85768:W16504
- 40 F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547:57//Hs.107474:AF045451
- F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121:64//Hs.2864:L40157
- 45 F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//4.9e-118:594:95//Hs.40820:AF058953
- 50 F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043
- F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:AF054179
- 55 F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161

EP 1 074 617 A2

- F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258
- 5 F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111
- F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144
- 10 F-NT2RP2004936
- F-NT2RP2004959
- 15 F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763
- 20 F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478
- F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735
- 25 F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927
- 30 F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.41723:U37426
- F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478
- 35 F-NT2RP2004999
- F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//Hs.124161:AF065164
- 40 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:AB014515
- 45 F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200
- F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141
- 50 F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600
- 55 F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433
- F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:

EP 1 074 617 A2

60//Hs.139745:U39067

5 F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:
D67035

10 F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:
60//Hs.58167:D30612

F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:
498:59//Hs.137574:AF055917

15 F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838

F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:
98//Hs.22616:AB014564

20 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)
//9.2e-29:157:98//Hs.100555:X98743

25 F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803

F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947

30 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-
91:447:96//Hs.132226:AF045583

35 F-NT2RP2005147

F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI357582

40 F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:
AI357868

F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:
96//Hs.155218:AJ007509

45 F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:
AJ012159

50 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:
95//Hs.8173:AC005189

55 F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783

F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264:U70439

EP 1 074 617 A2

F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341

5 F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs.81452:AF030555

10 F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI383932

F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//Hs.27007:AF060219

15 F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590

20 F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833

F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763:AB014576

25 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.6e-23:166:90//Hs.1569:U11701

30 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.016:353:62//Hs.113265:AF032387

F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138

35 F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958

40 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100:489:96//Hs.107254:AC005943

F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122

45 F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs.113252:U80761

50 F-NT2RP2005407

F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.28:338:57//Hs.6189:AB011133

55 F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068

F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164

EP 1 074 617 A2

- 5 F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE
SUBUNIT B14.5B [Bos taurus]//8.5e-48:295:90//Hs.75017:AA166853
- F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243
- 10 F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//0.032:176:
64//Hs.16:D10656
- F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:AD78412
- 15 F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds//9.9e-48:432:
77//Hs.15519:AB018315
- F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573
- 20 F-NT2RP2005491
- F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:AI084164
- 25 F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-48:621:68//Hs.6833:
AB002324
- 30 F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete cds//1.6e-
63:503:78//Hs.7688:M64930
- 35 F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.56:139:
66//Hs.8546:U97669
- F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase),
regulatory (30.8kD)//1.0:291:59//Hs.89709:L35546
- 40 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA,
complete cds//1.2e-82:444:92//Hs.119023:AF092563
- 45 F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//2.2e-19:112:
99//Hs.6232:AB018307
- 50 F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1
[H.sapiens]//3.5e-50:366:83//Hs.61833:AA036735
- F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//9.4e-155:747:
97//Hs.159597:AJ012449
- 55 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.9e-131:618:
98//Hs.62515:AB007963

EP 1 074 617 A2

F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10
 IN CHROMOSOME III [C.elegans]//2.5e-51:292:93//Hs.105684:H24407
 5 F-NT2RP2005555//EST//0.046:308:57//Hs.145962:AI276822
 F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:AI422839
 10 F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436
 F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:AI218627
 15 F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071
 F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:
 20 97//Hs.22396:AF062085
 F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702
 25 F-NT2RP2005635
 F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905
 30 F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:AI292145
 F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:AI375440
 35 F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.1433065:M86917
 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-08:351:
 40 62//Hs.91400:AB006626
 F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239
 F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete
 45 cds//7.7e-96:462:98//Hs.25664:AF089814
 F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702
 50 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79217:
 M77836
 55 F-NT2RP2005694
 F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA,
 complete cds//0.15:496:55//Hs.79326:L76703

EP 1 074 617 A2

- 5 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1e-126:599:97//Hs.61638:AB018342
- F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527
- 10 F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//Hs.69740:U09367
- F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017
- 15 F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:AI334191
- F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086
- 20 F-NT2RP2005741//Homo sapiens chondroadherin gene, 5'flanking region and//0.80:362:58//Hs.97220:U96769
- F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688
- 25 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//Hs.159651:AF068868
- 30 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.26285:AF082516
- 35 F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853
- F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895
- 40 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836
- 45 F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:Z50115
- F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556
- 50 F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.34853:U28368
- 55 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820
- F-NT2RP2005812

EP 1 074 617 A2

F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595

F-NT2RP2005835

5

F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//Hs.59829:AB014602

10

F-NT2RP2005853

F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:98//Hs.50758:AF092564

15

F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567

F-NT2RP2005868

20

F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240:L16782

25

F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943

F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360

30

F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399

F-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882:AA292186

35

F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770

F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339

40

F-NT2RP2006023

F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382

45

F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664

50

F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093

F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469

55

F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416

EP 1 074 617 A2

F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970

F-NT2RP2006100

5

F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135

F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349

10

F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240

F-NT2RP2006166

15

F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73//Hs.74368:
X69910

20

F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-114:567:
96//Hs.109299:AB014554

25

F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:
85//Hs.15519:AB018315

F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503

30

F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.153910:
X96484

F-NT2RP2006237

35

F-NT2RP2006238

F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970

40

F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//0.019:111:
71//Hs.157199:X97630

45

F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete
cds//2.4e-05:388:60//Hs.75111:D87258

50

F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:
97//Hs.3404:AF035262

55

F-NT2RP2006320//ESTs, Moderately similar to maternal transcript Maid [M.musculus]//1.9e-
29:151:100//Hs.36794:AI038407

F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371

EP 1 074 617 A2

F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:70//Hs.87202:D82344

5 F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892:AF076974

10 F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174

F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501

15 F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341

20 F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.95838:AF059734

F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934

25 F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509

F-NT2RP2006456

30 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein/1.1e-149:545:98//Hs.72160:AJ006266

F-NT2RP2006467

35 F-NT2RP2006472

F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048

40 F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134

45 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966

F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.73864:U22029

50 F-NT2RP2006573

F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223

55 F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180

F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-

EP 1 074 617 A2

137:637:98//Hs.6764:AJ011972

5 F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:
568:61//Hs.79531:AF000560

F-NT2RP3000047

10 F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete
cds//1.2e-58:633:69//Hs.37138:U35376

15 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961

F-NT2RP3000068

20 F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769

F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:
78//Hs.108287:L27670

25 F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:
X14608

30 F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140

F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595

35 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:438:
100//Hs.8173:AC005189

40 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:
98//Hs.13273:AB011164

F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-20:133:
94//Hs.23094:M19503

45 F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-
08:152:71//Hs.127338:AB007961

50 F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779

F-NT2RP3000207

55 F-NT2RP3000220

F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-
20:509:58//Hs.122967:AF059569

EP 1 074 617 A2

- F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740
- 5 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691:86//Hs.75863:D86972
- F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733
- 10 F-NT2RP3000252
- F-NT2RP3000255
- 15 F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568
- F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214:67//Hs.80261:L43821
- 20 F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863
- F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.0088:236:63//Hs.102732:U88153
- 25 F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:AI091242
- 30 F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.57:189:65//Hs.46146:AA418097
- F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390
- 35 F-NT2RP3000348
- 40 F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754
- F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642:X60673
- 45 F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921
- F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymnaea stagnalis]//4.0e-116:596:95//Hs.21094:AI337016
- 50 F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639
- 55 F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873

EP 1 074 617 A2

F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307:AF071185

5 F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610:65//Hs.23094:M19503

10 F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948

F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487

15 F-NT2RP3000441

F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:AI051562

20 F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.75562:U48705

F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068

25 F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:AI289822

F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058

30 F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667

F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379

35 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:63//Hs.79347:D86966

F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308

40 F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412

F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404

45 F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723

F-NT2RP3000578

50 F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277

F-NT2RP3000584

55 F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904

F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:57//Hs.77234:

EP 1 074 617 A2

AB001914

- 5 F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811
- F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:355:92//Hs.114622:AA693492
- 10 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:59//Hs.79170:D86980
- F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:AI421203
- 15 F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683
- F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162
- 20 F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:AI017333
- F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904
- 25 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.155464:AF088219
- 30 F-NT2RP3000661
- F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.13063:AF017789
- 35 F-NT2RP3000685
- F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001
- 40 F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884
- F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854
- 45 F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:AI369426
- F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765
- 50 F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245:91//Hs.2427:D89937
- 55 F-NT2RP3000815
- F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132

EP 1 074 617 A2

- F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700
- 5 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapiens]//1.1e-71:363:96//Hs.23803:AA126476
- 10 F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012
- F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593:68//Hs.157199:X97630
- 15 F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520
- F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:86//Hs.155464:AF088219
- 20 F-NT2RP3000852
- F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699918
- F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476
- 30 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766:60//Hs.15432:U53445
- F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60//Hs.79706:U53204
- 35 F-NT2RP3000875
- F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101
- 40 F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI348374
- F-NT2RP3000917
- 45 F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340:60//Hs.109895:X68277
- F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X84407
- 50 F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:AI204212
- F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411
- 55 F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N92198

EP 1 074 617 A2

F-NT2RP3001007

5 F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V)
chain [C.elegans]//2.9e-121:588:98//Hs.128781:AA160707

10 F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-
54:282:97//Hs.30303:AI244662

15 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete
cds//2.7e-51:534:74//Hs.27007:AF060219

F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474:
60//Hs.21264:AB018325

20 F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.4e-16:
428:60//Hs.155481:AJ006470

25 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:
64//Hs.82292:D86969

F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:AI337050

30 F-NT2RP3001111

F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088

35 F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023

F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779

40 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:
61//Hs.12107:AF042384

45 F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687:75//Hs.69740:
U09367

F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:
60//Hs.94790:AB018318

50 F-NT2RP3001133//Homeo box A4//0.00011:484:59//Hs.77637:M74297

55 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:
98//Hs.5378:AB018305

F-NT2RP3001147

EP 1 074 617 A2

F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605

5 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891:98//Hs.72160:
AJ006266

F-NT2RP3001176

10 F-NT2RP3001214//EST//0.88:218:60//Hs.161147:AI417859

F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W19981

15 F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512:
95//Hs.103816:AA130866

20 F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010

F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756

25 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:
L06237

F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132

30 F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:293:60//Hs.32934:
U27109

35 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:
64//Hs.107809:AB018269

40 F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain
polypeptide)//1.2e-42:454:72//Hs.41728:L75847

F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566

45 F-NT2RP3001274

F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811

50 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:
69//Hs.31463:D87457

55 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:
68//Hs.159437:U44060

F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen

EP 1 074 617 A2

debranching enzyme, glycogen storage disease type III)/0.012:522:56//Hs.904:U84010

F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731

5

F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966

10

F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:AB007920

15

F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.00019:473:61//Hs.124161:AF065164

F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831

20

F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487

25

F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022

F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451

30

F-NT2RP3001384//Homa sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332

35

F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595

F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783

40

F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.0e-05:189:66//Hs.41728:L75847

45

F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end//0.77:132:66//Hs.111024:L77567

F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658

50

F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047

F-NT2RP3001426

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F-NT2RP3001427

F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:431:91//Hs.85844:

EP 1 074 617 A2

X66397

5 F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
[H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393

F-NT2RP3001447

10 F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:
68//Hs.89631:U48508

F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212

15

F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323

F-NT2RP3001459

20

F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//4.2e-
10:168:70//Hs.32317:AF072836

25

F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877

F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231

30

F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8)
mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801

35

F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete
cds//9.4e-139:743:91//Hs.85283:U36500

40

F-NT2RP3001529//ESTs, Moderately similar to topoisomerase IC-terminal fragment
[H.sapiens]//0.28:224:65//Hs.105912:AI431328

F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074

45

F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.147918:U38291

F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:
X16302

50

F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
//0.049:185:65//Hs.1686:M69013

55

F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.6e-51:345:
82//Hs.144563:AF057280

F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688

EP 1 074 617 A2

- F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349
- 5 F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435
- F-NT2RP3001629
- 10 F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:276:97//Hs.9899:AF099149
- F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173
- 15 F-NT2RP3001646
- F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e-172:816:98//Hs.159597:AJ012449
- 20 F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027
- 25 F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [*Pseudomonas fluorescens*]//9.0e-53:375:85//Hs.41127:AA555184
- F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071
- 30 F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [*Caenorhabditis elegans*]//4.0e-111:518:99//Hs.20364:AI420022
- 35 F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198
- 40 F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329
- F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219
- 45 F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [*D.melanogaster*]//1.4e-31:191:94//Hs.131279:AA486291
- F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862
- 50 F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [*Mus musculus*]//7.6e-159:747:98//Hs.6823:W18181
- 55 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177

EP 1 074 617 A2

- 5 F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]/3.5e-116:554:98//Hs.144332:AA046836
- 10 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:78//Hs.90998:D50918
- 15 F-NT2RP3001739
- F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.116549:AL009172
- 20 F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.22138:U49250
- 25 F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2.4e-47:725:64//Hs.41688:U27193
- F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds//0.42:198:61//Hs.57783:U78525
- 30 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1e-153:710:98//Hs.28169:AB007928
- F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.79024:L03532
- 35 F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361
- F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L41162
- 40 F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379:58//Hs.32950:X82634
- 45 F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729
- F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.8e-35:481:67//Hs.158225:U68727
- 50 F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706
- 55 F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.elegans]/2.9e-94:452:98//Hs.54952:AA872675
- F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6139:AL022326

EP 1 074 617 A2

- F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896
- 5 F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185
- F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247
- 10 F-NT2RP3001931
- F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022:268:61//Hs.106070:U22398
- 15 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.8e-167:815:96//Hs.15869:AB014575
- 20 F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335
- F-NT2RP3001969
- 25 F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180
- F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs.155464:AF088219
- 30 F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.75087:X86779
- F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946
- 35 F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821
- F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67//Hs.147189:D88153
- 40 F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]//3.8e-48:353:81//Hs.127507:AA993745
- 45 F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0e-25:212:83//Hs.71622:AA195155
- 50 F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens]//4.2e-82:407:97//Hs.131888:AI091806
- 55 F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503
- F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710

EP 1 074 617 A2

- 5 F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//0.91:194:65//Hs.1298:J03779
- F-NT2RP3002081
- 10 F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA partial cds//0.073:297:61//Hs.102732:U88153
- F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256
- 15 F-NT2RP3002108
- F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018
- 20 F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260
- 25 F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009
- 30 F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644
- F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985
- 35 F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]//3.0e-61:340:93//Hs.11379:AA594140
- 40 F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046
- F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915
- 45 F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA30643
- 50 F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic1)//0.98:242:57//Hs.114001:Z20656
- F-NT2RP3002248
- 55 F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261
- F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete

EP 1 074 617 A2

cds//0.42:189:62//Hs.110637:AC004080

F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139

5

F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386

F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910

10

F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871

15

F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383

F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65:588:75//Hs.154672:X16396

20

F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//4.2e-166:770:98//Hs.6483:Y16355

25

F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200

30

F-NT2RP3002399

F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274

35

F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:AB014578

40

F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:AI291310

F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108

45

F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935

F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.57738:U35246

50

F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542:AB018272

55

F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510:70//Hs.96759:AA469984

EP 1 074 617 A2

- F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706
- 5 F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054
- F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919
- 10 F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508
- F-NT2RP3002603
- 15 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:61//Hs.3845:AB014888
- 20 F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.121287:AF029900
- F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.6e-13:441:63//Hs.155481:AJ006470
- 25 F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.151518:U38847
- 30 F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308
- F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70//Hs.41086:AI337400
- 35 F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI421991
- 40 F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:294:100//Hs.128750:AI367584
- F-NT2RP3002687
- 45 F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI352200
- F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI393657
- 50 F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279514
- F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291
- 55 F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161:62//Hs.129736:AF040753

EP 1 074 617 A2

F-NT2RP3002785

5 F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713

F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:423:93//Hs.41068:AA844350

10

F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940:AF004715

15 F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070

F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582

20 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895

F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040

25

F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314

30 F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765

F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//Hs.3826:U69560

35

F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599:AB011160

40 F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262

F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870

45

F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997

50 F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI287703

F-NT2RP3002985//Human TFIIIB related factor hBRF (HBRF) mRNA, complete cds//0.071:550:58//Hs.32935:U28838

55

F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308

EP 1 074 617 A2

F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083

5 F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446

F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749

10 F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609

F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928

15 F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079

F-NT2RP3003078

20 F-NT2RP3003101

F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!!
[H.sapiens]//0.98:88:68//Hs.99715:AA292700

25

F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740

30 F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative
receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.101299:AF017061

F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975

35 F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA,
complete cds//2.2e-20:430:63//Hs.118397:AF053944

F-NT2RP3003150

40

F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete
cds//2.0e-72:894:68//Hs.37138:U35376

45 F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:
59//Hs.6150:AB011093

F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:X78933

50

F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211

F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854

55

F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308

EP 1 074 617 A2

F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325

F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525

5

F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:D44497

10

F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:AF055460

F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200

15

F-NT2Rp3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//Hs.620:M69225

20

F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792:AF044924

25

F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983

F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953

30

F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947

F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503

35

F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947

F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058

40

F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200

F-NT2RP3003330

45

F-NT2RP3003344

F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339

50

F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833

55

F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542

EP 1 074 617 A2

F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791

5 F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:
H16363

F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850

10 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete
cds//3.2e-22:430:63//Hs.113272:U90653

15 F-NT2RP3003411//Human metallothionein-le gene (hMT-le)//0.99:116:62//Hs.74170:M10942

F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830

20 F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:
M93425

25 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-
182:853:98//Hs.14934:AF004828

F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:
98//Hs.26450:AB018268

30 F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98330

F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302

35 F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:
626:58//Hs.150828:AF038169

40 F-NT2RP3003552

F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:AI418322

45 F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365

F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311

50 F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247

F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56741

55 F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:
564:61//Hs.104:D14012

F-NT2RP3003625

EP 1 074 617 A2

- F-NT2RP3003656
- 5 F-NT2RP3003659
- F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586
- 10 F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184
- F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA,
complete cds//0.013:190:63//Hs.44585:U58334
- 15 F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246:
62//Hs.118463:AF055000
- 20 F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848
- F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:
61//Hs.48998:AB007865
- 25 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700:
98//Hs.48513:AB018300
- 30 F-NT2RP3003746
- F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230
- 35 F-NT2RP3003799
- F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog//4.7e-
41:432:73//Hs.1422:M19722
- 40 F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy,
hypertrophic 1)//0.98:242:57//Hs.114001:Z20656
- 45 F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA,
complete cds//5.1e-07:624:59//Hs.96028:AF042832
- 50 F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking
sequence//0.84:171:63//Hs.102877:U41315
- F-NT2RP3003825
- 55 F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:AI346481
- F-NT2RP3003831

EP 1 074 617 A2

- 5 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300:AF070611
- 10 F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:M73780
- 15 F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268
- 20 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738:AB018343
- 25 F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243:90//Hs.124832:AA846576
- 30 F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//1.1e-107:499:99//Hs.105794:AA701659
- 35 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49:404:77//Hs.9006:AF057358
- 40 F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396
- 45 F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006
- 50 F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta) //0.00070:433:58//Hs.93909:AF042498
- 55 F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//2.8e-127:617:97//Hs.142151:AA984061
- F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs.155302:U57317
- F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234
- F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:67//Hs.26441:AB002317
- F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875
- F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression) //5.3e-90:520:90//Hs.100007:X76091
- F-NT2RP3004093

EP 1 074 617 A2

- 5 F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258
- F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390
- 10 F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:AI096509
- F-NT2RP3004145
- 15 F-NT2RP3004148
- F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:AF032900
- 20 F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706
- F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640
- 25 F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:62//Hs.101047:M31523
- 30 F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835
- F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361
- 35 F-NT2RP3004242
- F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240
- 40 F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:AI149140
- F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067
- 45 F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.158471:AF088982
- 50 F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597:61//Hs.19261:AF007871
- 55 F-NT2RP3004332
- F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285

EP 1 074 617 A2

- F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426
- 5 F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999
- F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141429:AA631915
- 10 F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//4.3e-125:608:98//Hs.128781:AA160707
- 15 F-NT2RP3004399//H.sapiens mRNA for leucine-rich, primary response protein 1//2.3e-141:804:90//Hs.123122:X97249
- F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:96//Hs.20132:AA203113
- 20 F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.153638:AF010403
- 25 F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.00023:357:59//Hs.99948:M97016
- 30 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583:99//Hs.27349:AB007917
- 35 F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399:58//Hs.22616:AB014564
- F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219
- 40 F-NT2RP3004472
- F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715:98//Hs.5003:AB007925
- 45 F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//4.6e-118:547:99//Hs.124768:AA307735
- 50 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752:97//Hs.158311:AB012851
- 55 F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [M.musculus]//3.5e-89:425:99//Hs.126082:AI077718
- F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256

EP 1 074 617 A2

- 5 F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370:59//Hs.158244:AB007948
- F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.7647:M94046
- 10 F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110
- F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571
- 15 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679:98//Hs.75970:AB014532
- F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793:98//Hs.74750:AB011126
- 20 F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362:94//Hs.125870:AI364967
- 25 F-NT2RP3004569
- F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF50) mRNA, complete cds//3.3e-181:860:97//Hs.122752:AF026445
- 30 F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928:AB007923
- 35 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266
- 40 F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger protein, efp [H.sapiens]//6.4e-13:356:64//Hs.124138:AI266336
- F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232
- 45 F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204
- 50 F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436
- F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98//Hs.118991:AA675919
- 55 F-NT2RP4000023//ESTs//1-4e-33:182:96//Hs.122722:AA455668
- F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495

EP 1 074 617 A2

- 5 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761
- F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481:AJ006470
- 10 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720:97//Hs.159597:AJ012449
- F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743
- 15 F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538
- 20 F-NT2RP4000111
- F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:AB007952
- 25 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069
- 30 F-NT2RP4000150
- F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356
- 35 F-NT2RP4000159
- F-NT2RP4000167
- 40 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946
- F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:AB014600
- 45 F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006
- 50 F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731
- F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.46468:U45984
- 55 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481:AJ006470

EP 1 074 617 A2

- 5 F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:384:89//Hs.115498:AA436298
- F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:AF091092
- 10 F-NT2RP4000263
- F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580
- 15 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481
- F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.143648:AB000732
- 20 F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112
- 25 F-NT2RP4000355
- F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:AB018281
- 30 F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195
- 35 F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073
- 40 F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.098:291:59//Hs.994:M95678
- F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965
- 45 F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368
- 50 F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688
- F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156
- 55 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-

EP 1 074 617 A2

34:431:73//Hs.46468:U45984

5 F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087

F-NT2RP4000449//EST//0.84:113:65//Hs.145274:AI249468

10 F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853

15 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499

20 F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535

F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742

25 F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.159234:U89995

30 F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293

F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594

35 F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904

40 F-NT2RP4440518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:AJ010840

F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372

45 F-NT2RP4000524

F-NT2RP4000528

50 F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154

55 F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.25597:H93026

F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351

EP 1 074 617 A2

F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053

5 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete
cnds//1.0e-139:666:98//Hs.4214:AF067730

F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513

10 F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396

F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA,
complete cds//0.00056:367:60//Hs.144626:AF100907

15 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:
300856//8.0e-167:676:98//Hs.50748:AB004848

20 F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor
(NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783

25 F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:
78//Hs.111817:T80622

F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:
71//Hs.38176:AB011178

30 F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:
D87440

35 F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058

F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:
60//Hs.20912:AB012162

40 F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:
D42123

45 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:
98//Hs.25132:AB007939

50 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:
99//Hs.8173:AC005189

F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833

55 F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603

F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete

EP 1 074 617 A2

cds//1.4e-37:680:63//Hs.75875:U49278

5 F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367

F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:AI206803

10 F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843

F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142

15 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901

20 F-NT2RP4000918

F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

25 F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503

F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//Hs.24812:AF069532

30 F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371

35 F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542

40 F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888

F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058

45 F-NT2RP4000979

F-NT2RP4000984

50 F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913

55 F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068

F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204

EP 1 074 617 A2

F-NT2RP4001004

5 F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718

10 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.113287:AF009204

15 F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494

F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:L40157

20 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157

F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481:AJ006470

25 F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497

30 F-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase, partial//1.4e-131:634:98//Hs.106778:AJ010953

35 F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//0.025:166:66//Hs.146459:X66975

F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164

40 F-NT2RP4001095

45 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054

F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//2.2e-26:171:92//Hs.14038:R06800

50 F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142

55 F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:100//Hs.126925:AA931237

EP 1 074 617 A2

F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.1433 82:AA476266

F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261

5 F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207

F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171

10 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734

F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324

15 F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264

F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324

20 F-NT2RP4001207

F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636

25 F-NT2RP4001213//KRAB zinc finger protein {alternative products}//1.1e-45:187:74//Hs.22556:U37251

F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262

30 F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.122967:AF059569

35 F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778

40 F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463

F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59kD, acidic component)//0.015:246:62//Hs.31121:U40571

45 F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578

50 F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736

55 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250

EP 1 074 617 A2

- F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917
- 5 F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110
- F-NT2RP4001339
- 10 F-NT2RP4001343
- F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39;686:64//Hs.112125:M12625
- 15 F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//2.0e-31:784:62//Hs.15432:U53445
- F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356
- 20 F-NT2RP4001372
- 25 F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194
- F-NT2RP4001375
- 30 F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190
- F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918
- 35 F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109
- 40 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957
- F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:X78933
- 45 F-NT2RP4001442
- F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:AB018326
- 50 F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.26676:AA033997
- 55 F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523

EP 1 074 617 A2

- 5 F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN
[H.sapiens]//0.25:216:60//Hs.63220:AA522707
- F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395
- 10 F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:
61//Hs.5923:X82260
- F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:
15 AI377863
- F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:
76//Hs.154970:U03494
- 20 F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:
221:65//Hs.44481:U13220
- F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:
25 U50534
- F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174
- 30 F-NT2RP4001567
- F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-
CBR5 INTERGENIC REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:
35 AA167836
- F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410
- 40 F-NT2RP4001574
- F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:
45 AL031228
- F-NT2RP4001592
- F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903
- 50 F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952
- F-NT2RP4001634
- 55 F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKH1-
STH1 INTERGENIC REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436

EP 1 074 617 A2

- 5 F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409
- 10 F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629
- 15 F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162:67//Hs.30250:AF055376
- 20 F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080
- 25 F-NT2RP4001696
- 30 F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927
- 35 F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.92614:M62302
- 40 F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198
- 45 F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878
- 50 F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656
- 55 F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:AC004522
- F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069
- F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131
- F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:U11690
- F-NT2RP4001828
- F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888
- F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749

EP 1 074 617 A2

F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336:AB014572

5 F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//4.8e-12:84:94//Hs.140232:AA705170

10 F-NT2RP4001889

F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:97//Hs.15144:AC005014

15 F-NT2RP4001896

F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848

20 F-NT2RP4001927

F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.8e-54:375:84//Hs.119294:AI379442

25 F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894

30 F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063

F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868

35 F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:788:65//Hs.23796:AL022718 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete cds//0.0019:279:65//Hs.159439:AF092047

40 F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//0.58:463:55//Hs.3826:U69560

45 F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139

50 F-NT2RP4002052

F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873

55 F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//Hs.100030:AF002999

F-NT2RP4002075

EP 1 074 617 A2

- 5 F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.0e-38:243:90//Hs.139115:AA325104
- F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654
- 10 F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:M96684
- F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284
- 15 F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204
- F-NT2RP4002888
- 20 F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960
- F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96//Hs.74456:U34995
- 25 F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071
- 30 F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067
- F-NT2RP5003492
- 35 F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase, complete cds//6.1e-56:750:69//Hs.132884:AB006179
- 40 F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-14:348:62//Hs.154050:AC004131
- F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.94:202:63//Hs.8152:AB014542
- 45 F-NT2RP5003522
- 50 F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943
- F-NT2RP5003534
- 55 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0e-69:373:94//Hs.108258:AB007934

EP 1 074 617 A2

F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729

5 F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina moschata]//4.4e-75:355:99//Hs.36727:AI051983

F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304

10 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:815:98//Hs.81449:AF058922

15 F-OVARC1000017//Homo sapiens mRNA for NTAk, complete cds//0.50:482:58//Hs.113264:AB005060

F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:238:89//Hs.69469:AF064603

20

F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549

25 F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapiens]//6.7e-60:305:97//Hs.31696:H50008

F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798

30 F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543

F-OVARC1000085

35 F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442

F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete . cds//0.00017:414:59//Hs.106387:AF029778

40

F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600

45 F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]//2.9e-73:406:92//Hs.109463:AI205174

F-OVARC1000109

50 F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250

55 F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.4e-43:532:72//Hs.118401:AB011134

F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010

EP 1 074 617 A2

F-OVARC1000139

5 F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293

F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414

10 F-OVARC1000151

F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305

15 F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)//0.10:504:59//Hs.154083:U70136

F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131

20 F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840

F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834

25 F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//2.7e-31:264:79//Hs.151895:AA196379

30 F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984

F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.00084:170:65//Hs.107747:AI357868

35 F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306

40 F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287

F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECURSOR [Felis catus]//0.51:193:66//Hs.6194:AI378579

45 F-OVARC1000321

F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60//Hs.122359:AF051946

50 F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444

55 F-OVARC1000347

F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha

EP 1 074 617 A2

subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450

5 F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64//Hs.156016:D50930

F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162

10 F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682

F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58//Hs.156016:D50930

15 F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7e-25:190:84//Hs.139513:AA259082

20 F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615

F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93 :281:60//Hs.76279:X53416

25 F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//Hs.83987:U09284

30 F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423

F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.2e-140:566:99//Hs.12334:AB014583

35 F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:AI024524

F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.108112:AF070640

40 F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854

45 F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926

F-OVARC1000479

50 F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036

F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327

55 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:539:99//Hs.111285:AF051850

F-OVARC1000526//ESTs//2.9e-08:368:611//Hs.42771:N26740

EP 1 074 617 A2

F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492

5 F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475

F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667

10 F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410

F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135:66//Hs.85302:U76421

15 F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358

F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200

20 F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729

F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63//Hs.3080:U29725

25 F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722

30 F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881

F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097

35 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds//1.6e-78:424:93//Hs.86859:D43772

F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536:94//Hs.111862:AB011162

40 F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:AI277106

45 F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279

F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639

50 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549:99//Hs.125315:AF027156

55 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306

F-OVARC 1000700

EP 1 074 617 A2

F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320

5 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//1.2e-110:451:91//Hs.13476:AF038661

10 F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318:91//Hs.7049:AI141736

F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411

15 F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196

F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194:99//Hs.157059:W28130

20 F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793

F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835

25 F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584

F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032

30 F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390

F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432:100//Hs.155995:AB014543

35 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//Hs.18910:AF045584

40 F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6.1e-31:183:93//Hs.108620:AA418155

45 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133:69//Hs.159234:U89995

50 F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143

F-OVARC1000885//EST//0.91:152:63//Hs.160765 :AI313323

55 F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777

F-OVARC 1000890

EP 1 074 617 A2

F-OVARC1000891

5 F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818

F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:AI376601

10 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419:97//Hs.9028:AF039691

F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456

15 F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623:72//Hs.114440:M11119

F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078

20 F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157:97//Hs.136243:AA307843

25 F-OVARC 1000948

F-OVARC1000959//EST//0.65:293:55//Hs.134725:AI088986

30 F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952

F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288

35 F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:AI283069

F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661

40 F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs.155302:U5 7317

45 F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458:AF088219

F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114

50 F-OVARC1001004

F-OVARC1001010

55 F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234:99//Hs.110327:AA205866

EP 1 074 617 A2

F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.0076:624:57//Hs.75063:AL023584

5 F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578:89//Hs.111974:AI050735

10 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733:97//Hs.9899:AF099149

F-OVARC 1001040//ESTs//2.2e-38:204:96//Hs.128927:AI168074

15 F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385

F-OVARC1001051

20 F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381:81//Hs.154968:U02020

25 F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:AI312873

F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183:84//Hs.46680:AA809451

30 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620:98//Hs.3426:AF082657

35 F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013

F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937

40 F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X98248

F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.3e-75:289:95//Hs.21753:AJ005897

45 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//Hs.12912:AF015913

50 F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.1e-151:710:98//Hs.26584:AF051782

55 F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102

F-OVARC1001118

EP 1 074 617 A2

F-OVARC1001129

F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008

5 F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725

F-OVARC1001162

10 F-OVARC1001167

F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:AI078279

15 F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287

F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159

20 F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1
 PRECURSOR [Homo sapiens]//1.8e-11:192:69//Hs.130020:AA887581

25 F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:
 58//Hs.91103:AC005551

F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//1.5e-13:199:
 30 71//Hs.109966:C06057

F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-
 RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324:90//Hs.114673:W72675

35 F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889

F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X51688

40 F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745676

F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424825

45 F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.75243:D42040

F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:AI377837

50 F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821

F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224

55 F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8e-144:644:
 96//Hs.155995:AB014543

EP 1 074 617 A2

F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:355:60//Hs.108812:AA044835
 5 F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172
 F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete
 10 cds//0.20:188:64//Hs.152455:AF044209
 F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264
 15 F-OVARC1001330
 F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)//0.021:232:62//Hs.79410:U62531
 20 F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:363:99//Hs.105837:AA536054
 25 F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA897493
 F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:N67251
 30 F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198:61//Hs.105940:AF004715
 F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:AI264633
 35 F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:AI025777
 F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533:74//Hs.109299:AB014554
 40 F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365:73//Hs.129735:AF010144
 45 F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//4.1e-149:683:99//Hs.151428:AJ224819
 50 F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.097:235:65//Hs.25674:AF072242
 55 F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28225
 F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651

EP 1 074 617 A2

- F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586:69//Hs.74597:U52426
- 5 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651
- F-OVARC1001436
- 10 F-OVARC1001442
- F-OVARC1001453
- 15 F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.110950:AI041823
- 20 F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568
- F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343
- 25 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//2.6e-86:479:92//Hs.6534:AF016507
- F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-97:538:92//Hs.75813:L33243
- 30 F-OVARC1001525
- 35 F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786
- F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595
- 40 F-OVARC1001555
- F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA//6.8e-57:275:98//Hs.155160:AF031166
- 45 F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.0035:271:60//Hs.108465:AI144299
- 50 F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:216:99//Hs.120002:AI038398
- 55 F-OVARC1001611
- F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500

EP 1 074 617 A2

F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144

5 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582:AB006867

10 F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229

F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858

15 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807

F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863

20 F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825

F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588

25 F-OVARC1001762

F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.4e-150:706:98//Hs.155377:U97670

30 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:AB014575

35 F-OVARC 1001768//ESTs//0.035:179:64//Hs.87279:AI218697

F-OVARC1001791

40 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830

F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI005102

45 F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:AB018287

50 F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.69949:M94172

F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825

55 F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453

F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567

EP 1 074 617 A2

F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537

5 F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973

F-OVARC1001861

10 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611

F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709

15 F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127

20 F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953

F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.6e-57:300:96//Hs.6216:AF061749

25 F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834

30 F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261

F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263

35 F-OVARC1001928

F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204

40 F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794

45 F-OVARC1001949//KRAB zinc finger protein {alternative products}//1.8e-17:294:67//Hs.22556:U37251

F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228

50 F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639

F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-23:213:78//Hs.105292:AA504776

55 F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417

EP 1 074 617 A2

F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:
 98//Hs.108258:AB007934
 5
 F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865
 F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063
 10
 F-OVARC1002107
 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:
 15 498:96//Hs.75258:AF054174
 F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913
 20 F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:
 62//Hs.112725:AF056022
 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795
 25 F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097
 F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:
 30 58//Hs.107747:AI357868
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:
 35 64//Hs.118929:X79568
 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:
 64//Hs.108447:AJ000517
 40 F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230
 F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:AI378928
 45 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial
 cds//1.2e-52:550:72//Hs.42400:AF022789
 F-PLACE1000014
 50 F-PLACE1000031
 F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088
 55 F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494

EP 1 074 617 A2

F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755

F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499

5

F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-47:266:93//Hs.30026:AI356771

10

F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-15:203:70//Hs.157422:R85366

15

F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30:324:60//Hs.76460:U49082

F-PLACE1000094

20

F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//Hs.111081:AI380378

25

F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:AA632135

30

F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.151017:AF058291

F-PLACE1000185

35

F-PLACE1000213

F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255

40

F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226

F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022

45

F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202

F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294

50

F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047

F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675

55

F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197

EP 1 074 617 A2

F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153

5 F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024

F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516

10

F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260

15 F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174

20 F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053

F-PLACE1000424

25 F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590

F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//2.7e-52:421:80//Hs.69747:M35531

30

F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638

35 F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60//Hs.153014:AB002353

40

F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573

45 F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.75578:M85289

F-PLACE1000562

50 F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538

F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//Hs.21838:AF038179

55

F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542

EP 1 074 617 A2

- 5 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597:AJ012449
- F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751
- 10 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542
- F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986
- 15 F-PLACE1000636
- F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.0e-154:747:96//Hs.5819:AF102265
- 20 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.29595:AJ005896
- 25 F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353
- F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949
- 30 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447
- 35 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288
- F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:331:57//Hs.37110:U10694
- 40 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858
- F-PLACE1000769
- 45 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921:AB014548
- 50 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215
- F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079
- 55 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189

EP 1 074 617 A2

F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180

5 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:
U80736

F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000

10 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428

F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455

15 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201

F-PLACE1000948

20 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete
cds//7.9e-10:294:66//Hs.80261:L43821

25 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk28h2.5
[C.elegans]//9.3e-45:309:88//Hs.13531:R61789

F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.8597:L11672

30 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:
96//Hs.158497:AB018267

35 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913

F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:
61//Hs.1974:M92432

40 F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6940:Z48633

F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876

45 F-PLACE1001024

F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741

50 F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:
U53204

55 F-PLACE1001062

F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859

EP 1 074 617 A2

F-PLACE1001088

5 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485

F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817

10 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:71//Hs.150406:AF022158

15 F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704

F-PLACE1001168

20 F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135

25 F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741

F-PLACE1001238

30 F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494

F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929

35 F-PLACE1001272//COATOMER BETA'SUBUNIT//0.012:50:96//Hs.75724:X70476

F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283

40 F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:58//Hs.124161:AF065164

45 F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1) //0.91:221:61//Hs.16533:D87930

F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:370:60//Hs.42672:AF016052

50 F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385

F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591

55 F-PLACE1001351

F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8e-26:155:

EP 1 074 617 A2

95//Hs.61638:AB018342

5 F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44:393:79//Hs.152005:AF009615

F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748

10 F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09:117:84//Hs.21301:AF093419

15 F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646

F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete

20 CDS//0.0038:496:57//Hs.97681:AJ223333

25 F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.154069:U06452

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404:AF091087

30 F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232

F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987

35 F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510

F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455

40 F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716

F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529

45 F-PLACE1001503

F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914

50 F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753

F-PLACE1001545

55 F-PLACE1001551

F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835

EP 1 074 617 A2

- 5 F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233
- F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987
- 10 F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230
- F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005
- 15 F-PLACE1001611//Human faciogenital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690
- F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:AB018341
- 20 F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198
- 25 F-PLACE1001640
- F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927
- 30 F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250
- F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI125696
- 35 F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.101555:U93869
- 40 F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776
- 45 F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686
- F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094
- 50 F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.1480:M60052
- F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159
- 55 F-PLACE1001745

EP 1 074 617 A2

F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361

5 F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//2.8e-160:
773:97//Hs.4812:AF061243

10 F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-35:269:
83//Hs.5247:AF029750

F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283

15 F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, complete cds//3.4e-
52:548:72//Hs.150981:U47050

F-PLACE1001781

20 F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115

F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138

25 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS)
mRNA, partial cds//3.6e-110:546:96//Hs.40820:AF058953

F-PLACE1001821

30 F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494

F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214

35 F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906

F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257

40 F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220

F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-
45 153:685:95//Hs.17839:AF099936

F-PLACE1001928//H.sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837

50 F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:
58//Hs.106387:AF029778

F-PLACE1001989

55 F-PLACE1002004

EP 1 074 617 A2

F-PLACE1002046

5 F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108

F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555

10 F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178

15 F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//Hs.5171:AF069765

20 F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637

F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831

25 F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:75//Hs.144290:T61747

30 F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631

F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390

35 F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891

F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627

40 F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674

F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.90798:U79289

45 F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989

50 F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI024442

F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935

55 F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-75:434:83//Hs.23094:M19503

EP 1 074 617 A2

F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675

F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279

5 F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291

F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710

10 F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067

F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete
15 cds//2.6e-23:458:66//Hs.40993:AF000148

F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI368947

20 F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA,
complete cds//7.1e-07:270:66//Hs.150406:AF022158

F-PLACE1002465

25 F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:
AJ007581

30 F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523

F-PLACE1002493

35 F-PLACE1002499

F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete
40 cds//4.3e-19:708:59//Hs.111967:U76010

F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482

45 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:
95//Hs.88756:AB018256

F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566:
50 96//Hs.99348:AC004774

F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369

55 F-PLACE1002571//Homo sapiens mRNA for TP53, complete cds//0.99:274:59//Hs.138202:
AF027866

F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627

EP 1 074 617 A2

- F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI393725
- 5 F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:D44497
- F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187
- 10 F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI198915
- F-PLACE1002625
- 15 F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04412
- F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706
- 20 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:804:97//Hs.124903:AF068180
- 25 F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903
- F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:U92971
- 30 F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080
- F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728
- 35 F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827
- F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:AF082516
- 40 F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:AI368926
- 45 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994
- F-PLACE1002815
- 50 F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691
- 55 F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:AI089163
- F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:AI334167

EP 1 074 617 A2

- F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405
- 5 F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024
- F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627
- 10 F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:AI040029
- F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056
- 15 F-PLACE1002962
- F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:AI041815
- 20 F-PLACE1002991
- F-PLACE1002993
- 25 F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans]//1.3e-12:104:86//Hs.124808:T86959
- 30 F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:AB007979
- F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632:97//Hs.129872:AB011088
- 35 F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7e-14:555:58//Hs.154740:AB014567
- 40 F-PLACE1003045
- F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491
- 45 F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//Hs.102137:U31875
- 50 F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419
- F-PLACE1003136
- 55 F-PLACE1003145
- F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590

EP 1 074 617 A2

F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997

5 F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797

F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA,
complete cds//0.98:221:60//Hs.139756:U59209

10 F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532

F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:AI208770

15 F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208

F-PLACE1003249//Insulin-like growth factor 1 (somatomedia C)//0.99:175:62//Hs.85112:
X57025

20 F-PLACE1003256

F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802

25 F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106

F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete
cds//4.3e-51:700:67//Hs.37138:U35376

30 F-PLACE1003334

35 F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308

F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568

40 F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3)
mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715

45 F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei
brucei]//8.9e-35:332:78//Hs.163820:H71277

F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:
57//Hs.143897:AF075575

50 F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858

55 F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009

F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069

EP 1 074 617 A2

F-PLACE1003383

5 F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:94//Hs.125175:AI142546

F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178

10

F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.40:206:62//Hs.30223:X90846

15 F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912

F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874

20 F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635

F-PLACE1003516//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.4e-85:357:86//Hs.103948:K00627

25

F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145

F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:Z48633

30

F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248

35 F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543:97//Hs.120416:AA057428

F-PLACE1003553

40

F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780

F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367

45

F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932

F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194

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F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620

55

F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965

F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961

EP 1 074 617 A2

F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:
 97//Hs.56851:D83200
 5
 F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:
 64//Hs.22116:AF064104
 10
 F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896
 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:
 87//Hs.23094:M19503
 15
 F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105
 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762
 20
 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:
 58//Hs.158275:AI365413
 25
 F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:
 AB002299
 30
 F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:
 669:95//Hs.98658:AF053305
 F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101
 35
 F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor protein//8.5e-09:
 393:60//Hs.103527:AJ000553
 40
 F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:
 260:99//Hs.102928:AI346344
 F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648
 45
 F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983
 F-PLACE1003768//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.7e-40:608:
 68//Hs.139107:K00629
 50
 F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944
 55
 F-PLACE1003783
 F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:
 57//Hs.62318:AB018308

EP 1 074 617 A2

- 5 F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169
- F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786
- 10 F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165
- F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124
- 15 F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359
- F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257
- 20 F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770
- F-PLACE1003886
- 25 F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:D42108
- F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050
- 30 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944
- F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142
- 35 F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069
- 40 F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585
- F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537
- 45 F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536
- F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522:71//Hs.3136:U42412
- 50 F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812
- F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940
- 55 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516

EP 1 074 617 A2

F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene
spi1//0.85:164:64//Hs.153045:X52056

5 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-
41:422:74//Hs.3620:X04526

10 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:
AI333779

F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552

15 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:
D83785

F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666

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F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201

25 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor,
mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493

F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722

30

F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273

F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689

35

F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-
98:479:97//Hs.31718:N29128

40

F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:
U80736

F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:
56//Hs.154139:AB007914

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F-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete
cds//2.0e-157:756:97//Hs.127007:AF084830

50

F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884

F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576

55

F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:

EP 1 074 617 A2

94//Hs.11171:Y11588

F-PLACE1004336

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F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153

10

F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552

15

F-PLACE1004384//Human HsLIM15 mRNA for HsLim15, complete cds//2.0e-49:466:76//Hs.37181:D64108

F-PLACE1004388

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F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871

F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579

25

F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190

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F-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.9e-131:536:99//Hs.155410:U49283

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F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867

F-PLACE1004460

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F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363

F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085

45

F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416

F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163

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F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680

F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699:97//Hs.122752:AF026445

55

F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150

EP 1 074 617 A2

F-PLACE1004518

F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314

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F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854

10

F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371

F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299

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F-PLACE1004645

F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991

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F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590

F-PLACE1004664

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F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563

30

F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035606

35

F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589

F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561

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F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131

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F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845

F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542

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F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891

F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148

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F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680

F-PLACE1004743

EP 1 074 617 A2

F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]/2.0e-41:260:90//Hs.6863:W52470

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F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-172:828:97//Hs.104715:AF084367

10

F-PLACE1004777//Human myosin IXb mRNA, complete cds//1.0e-29:556:63//Hs.159629:U42391

F-PLACE1004793

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F-PLACE1004804

F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340

20

F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]/2.4e-78:415:95//Hs.80965:AA493284

25

F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:69//Hs.22111:AB002362

F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047

30

F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943

F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97669

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F-PLACE1004838

F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X80910

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F-PLACE1004868

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F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772

F-PLACE1004900

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F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382

F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929

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F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs.118910:U82130

EP 1 074 617 A2

- 5 F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839:AF099936
- 10 F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592
- 10 F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851
- 10 F-PLACE1004969
- 15 F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:235:60//Hs.27610:U34605
- 20 F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:AB011147
- 20 F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520
- 25 F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831
- 25 F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459
- 30 F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159
- 30 F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943
- 35 F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594
- 35 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:AB011148
- 40 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757:56//Hs.122967:AF059569
- 45 F-PLACE1005077//EST//0.79:283:591//Hs.89276:AA283899
- 45 F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740
- 50 F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:AB011147
- 55 F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401
- F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//8.9e-18:538:62//Hs.104640:AF000561

EP 1 074 617 A2

- 5 F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:
U76366
- F-PLACE1005111//ESTs//0.66:191:63//Hs.106446:N93227
- 10 F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661
- F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360:
63//Hs.142177:H11741
- 15 F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:
72//Hs.154326:D42087
- F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:
20 60//Hs.128316:AB014541
- F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.elegans]//4.4e-126:
583:99//Hs.25347:AI138605
- 25 F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417
- F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009
- 30 F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47-1
[D.melanogaster]//0.56:192:60//Hs.47334:W72370
- 35 F-PLACE1005243
- F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941
- 40 F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252
- F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:
98//Hs.118087:AB011182
- 45 F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947
- F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:
50 66//Hs.101642:X60673
- F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//0.83:239:
62//Hs.80684:X62534
- 55 F-PLACE1005313

EP 1 074 617 A2

F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.elegans]//6.0e-81:459:91//Hs.146177:R51650

5 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794

10 F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.96:510:56//Hs.159183:AB018297

F-PLACE1005373

15 F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348

F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751

20 F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951

F-PLACE1005467//HOMEODOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433

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F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925

30 F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5e-126:744:87//Hs.23094:M19503

F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323

35 F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA707973

F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029

40 F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105

F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747

45 F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572

F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335

50 F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385

F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144

55 F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:W81261

EP 1 074 617 A2

F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278

F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436

5

F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594

F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851

10

F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057

15

F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234

F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867

20

F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991

F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:AF083255

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F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618

30

F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:AB007917

35

F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457

F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437

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F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944

F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//Hs.75111:D87258

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F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302

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F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI125696

F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493

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F-PLACE1005802

EP 1 074 617 A2

F-PLACE1005803

5 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315:AF027156

10 F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:AF065482

F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//4.1e-42:327:81//Hs.138404:R70986

15 F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58//Hs.75770:L41870

20 F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497

F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905

25 F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242

F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487

30 F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552

F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300

35 F-PLACE1005898

F-PLACE1005921

40 F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504

F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274

45 F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342:57//Hs.89839:M18391

F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142

50 F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:X69978

F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357

55 F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468

F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:66//Hs.107747:

EP 1 074 617 A2

AI357868

5 F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, complete
cds//1.0:215:63//Hs.7885:U13948

F-PLACE1005968

10 F-PLACE1005990

F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:
77//Hs.42674:U61981

15

F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256

F-PLACE1006011

20

F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743

25 F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:
64//Hs.158319:AB018332

F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:
X99906

30

F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395

35 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:
679:99//Hs.4976:AF039023

F-PLACE1006129

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F-PLACE1006139

F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:
79//Hs.153014:AB002353

45

F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.sapiens]//2.9e-12:
119:84//Hs.23153:R92857

50

F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868

F-PLACE10061641/ESTs//0.099:223:60//Hs.8108:AA902721

55

F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:
92//Hs.152894:AC005239

EP 1 074 617 A2

F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:AI074005

5 F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464:AF091433

F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608

10 F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369:88//Hs.135623:AA134719

F-PLACE1006205

15

F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]//0.0089:166:63//Hs.127179:AI279486

20 F-PLACE1006225

F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668

25 F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185

F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802

30 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3e-168:791:98//Hs.31921:AB014548

F-PLACE1006262

35

F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.7277:AJ001625

40 F-PLACE1006318

F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503

45 F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:AI361492

F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249

50 F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481

F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.153529:AF070581

55

F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403:61//Hs.105940:AF004715

EP 1 074 617 A2

F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693

5 F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:97//Hs.22396:AF062085

10 F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:74//Hs.21560:AB002296

15 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.131846:AF069735

F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:AB011129

20 F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866

25 F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381

F-PLACE1006470

30 F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194

35 F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511

F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493

40 F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584

F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542

45 F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358

F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:AI356219

50 F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784

55 F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529

F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:

EP 1 074 617 A2

65//Hs.17630:AB018280

5 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781:99//Hs.155377:U97670

F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088

10 F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858

F-PLACE1006629//Homo sapiens (clone s22i71) mRNA fragment//0.097:229:63//Hs.26956:L40396

15 F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:AI131473

20 F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12:113:83//Hs.3385:N25917

F-PLACE1006678

25 F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153638:AF010403

30 F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382:63//Hs.43627:U35612

F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354

35 F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152

F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M97252

40 F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:AI075783

F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:AI051228

45 F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84:95//Hs.123642:M83941

50 F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:AI422017

F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892

55 F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403:56//Hs.15832:AB014518

F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103:619:

EP 1 074 617 A2

87//Hs.23094:M19503

- 5 F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876
- F-PLACE1006860//EST//0.0062:206:65//Hs.158793:AI376773
- 10 F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273
- F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268:58//Hs.5333:AB018254
- 15 F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601
- F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI089187
- 20 F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443
- F-PLACE1006917
- 25 F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913
- F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211
- 30 F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565
- F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127:L12723
- 35 F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]//3.2e-07:67:98//Hs.21806:AA630312
- F-PLACE1006962//H.sapiens ir1B mRNA//2.3e-16:202:71//Hs.135202:X63417
- 40 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:191:67//Hs.8813:AF032922
- 45 F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753
- F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//3.1e-05:594:58//Hs.32951:AF034102
- 50 F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971
- 55 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775:84//Hs.23094:M19503
- F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.129811:

EP 1 074 617 A2

AJ223957

- 5 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.75813:L33243
- F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987
- 10 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.18:268:63//Hs.904:U84010
- F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385
- 15 F-PLACE1007112
- F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:AI160121
- 20 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601
- 25 F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965
- F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669
- 30 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204
- 35 F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//2.0e-58:405:87//Hs.80598:D50495
- F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141
- 40 F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467
- F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909
- 45 F-PLACE1007274
- 50 F-PLACE1007276//ATPase, Cu⁺⁺ transporting, alpha polypeptide (Menkes syndrome)//0.94:167:64//Hs.606:L06133
- F-PLACE1007282
- 55 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436

EP 1 074 617 A2

F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412

5 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA, complete
cds//0.88:298:58//Hs.144877:AF029403

F-PLACE1007342

10 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA,
complete cds//1.7e-121:567:98//Hs.76596:AF096870

15 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:
X98173

F-PLACE1007375

20 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642

F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287

25 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial
sequence//3.8e-18:128:92//Hs.14387:AF093771

F-PLACE1007416

30

F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436

F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359

35

F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93//Hs.6445:
L40391

40 F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714

F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103

45 F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975

F-PLACE1007488

50 F-PLACE1007507//ESTs//1.2e-99:27 4:98//Hs.123462:AA903385

F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503

55 F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296

F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979

EP 1 074 617 A2

- 5 F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468:57//Hs.113283:AF018080
- F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:AI076755
- 10 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733:71//Hs.65238:AB014561
- F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863
- 15 F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257
- F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI089163
- 20 F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778:56//Hs.33010:AB014533
- F-PLACE1007621
- 25 F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867
- F-PLACE1007645
- 30 F-PLACE1007649
- F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266
- 35 F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI027055
- F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:AI348503
- 40 F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63//Hs.1103:X02812
- 45 F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.75789:D87953
- F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709:97//Hs.4812:AF061243
- 50 F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233:89//Hs.108797:AA476815
- 55 F-PLACE1007729//ESTs, Moderately similar to RETRO VIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:64//Hs.104129:AA923278

EP 1 074 617 A2

F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121:AB014585

5 F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424

10 F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030

F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:AI089469

15 F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656

F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504

20 F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107

F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841

25 F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261635

F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396:77//Hs.23094:M19503

30 F-PLACE1007852

F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020:AB018309

35 F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:AI038387

40 F-PLACE1007877

F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943

45 F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs.92381:AB007956

F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002

50 F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538

F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.5671:AF084530

55 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:730:98//Hs.78106:AF079529

EP 1 074 617 A2

F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:
 264:92//Hs.42222:W28567
 5 F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:AI097043
 F-PLACE1008000//Homo sapiens vcl 1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:
 10 AF087693
 F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031
 15 F-PLACE1008044
 F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382
 20 F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:
 151:71//Hs.159437:U44060
 F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:
 25 58//Hs.155494:U60975
 F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete
 30 cds//0.034:497:58//Hs.100431:AF044197
 F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769
 F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874
 35 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI218683
 F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1
 40 [M.musculus]//5.1e-20:124:95//Hs.146238:AI263135
 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427
 45 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524
 F-PLACE1008201
 50 F-PLACE1008209
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856
 55 F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:
 L13385

EP 1 074 617 A2

F-PLACE1008273

F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113

5

F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970

10

F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287

F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071

15

F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129

20

F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362

F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579

25

F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569

30

F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911

F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171

35

F-PLACE1008398

F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:62//Hs.25674:AF072242

40

F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326

45

F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943

F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653

50

F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499

55

F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, epidermoid

EP 1 074 617 A2

carcinoma cell line A431, mRNA, 3 genes, 1718 nt//0.019:530:58//Hs.72248:S72487

F-PLACE1008437

5

F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335

F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901

10

F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63//Hs.27590:AB002381

15

F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:U10886

20

F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TASK) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823

F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI274697

25

F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081

F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-45:507:71//Hs.8003:AC004997

30

F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.0:95:71//Hs.117546:U31767

35

F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:AI283069

F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175:812:98//Hs.23255:AB018334

40

F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350:66//Hs.151087:AA649326

45

F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794

F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560

50

F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458

F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211

55

F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394

F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535

EP 1 074 617 A2

- 5 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete
cgs//3.5e-135:622:99//Hs.147967:AF044333
- F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728
- 10 F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8,
23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete
cgs//8.3e-25:137:97//Hs.90443:AF038406
- F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741
- 15 F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080
- F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285:
20 69//Hs.35460:H65503
- F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:
25 503:97//Hs.6458:AF060543
- F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:
68//Hs.111380:AA258772
- 30 F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542
- F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA,
complete cds//6.7e-104:376:98//Hs.7179:AF011905
- 35 F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883
- F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2
40 HOMOLOG [Plasmodium falciparum (isolate k1 / thailand)]//0.73:354:59//Hs.26322:AA156858
- F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:AI052728
- 45 F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:AI221563
- F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:
50 68//Hs.23094:M19503
- F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323
- 55 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:
98//Hs.62318:AB018308
- F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W84771

EP 1 074 617 A2

F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026

5 F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937

F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:
625:58//Hs.24644:U75308

10 F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950

F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:
15 AJ003112

F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762

20 F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689

F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:
100//Hs.119689:S70585

25 F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:AI239698

F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:AI090525

30 F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800

F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091

35 F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:AI337031

F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011

40 F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:AI040890

F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788

45 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3)
mRNA, complete cds//1.1e-139:671:97//Hs.99742:AF035586

50 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:
59//Hs.35804:D25215

F-PLACE1009150//Human HsLIM15 mRNA for HsLimf5, complete cds//1.7e-50:440:
55 78//Hs.37181:D64108

F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-

EP 1 074 617 A2

46:440:69//Hs.158095:AB007953

5 F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:
245:61//Hs.92614:M62302

F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250

10 F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770

F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:AI282821

15 F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100

F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//3.6e-117:
20 588:95//Hs.54943:Z78396

F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689

25 F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131

F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:
77//Hs.146403:M29540

30 F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575

F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35
35 [Saccharomyces cerevisiae]//1.9e-21:121:98//Hs.124768:AA307735

F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338

40 F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA,
complete cds//9.7e-08:411:59//Hs.23731:U83192

F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594:
45 86//Hs.23094:M19503

F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767

50 F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473

F-PLACE1009368

55 F-PLACE1009375

F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81//Hs.43681:
AL022394

EP 1 074 617 A2

- F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M27878
- 5 F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101174:
AF047863
- 10 F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210:
86//Hs.3404:AF035262
- 15 F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:
68//Hs.155291:D13630
- F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:58//Hs.82128:
AJ012159
- 20 F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.76987:
AF012872
- 25 F-PLACE1009459//H.sapiens gap gene mRNA, complete CDS//1.0:241:60//Hs.151641:
Z24680
- 30 F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE
PHOSPHODIESTERASE BETA 2//0.00039:347:60//Hs.994:M95678
- F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A//4.1e-91:
464:96//Hs.155049:AC004531
- 35 F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:AI308839
- 40 F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:
63//Hs.16165:AB002405
- F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:
U70728
- 45 F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417
- F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:AI416956
- 50 F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866
- F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291
- 55 F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806
- F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:

EP 1 074 617 A2

66//Hs.13889:AI341394

5 F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080

F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:AI074011

10 F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:AI094085

F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773

15 F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087

F-PLACE1009639

20 F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:AB011159

25 F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494

F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534

30 F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926

35 F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650

F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789

40 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024

F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989

45 F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-130:600:95//Hs.16411:AL030996

55 F-PLACE1009845

F-PLACE1009861

EP 1 074 617 A2

F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021

5 F-PLACE1009886

F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889

10 F-PLACE1009908

F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717

15 F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379

F-PLACE1009925

20 F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153

F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446

25 F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345

F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114

30 F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540

35 F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:AB014529

F-PLACE1010023

40 F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878

F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.142151:AA984061

45 F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596

50 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:AF065482

F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424

55 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925

EP 1 074 617 A2

- 5 F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL
HYDROLASE [Mus musculus]//1.8e-38:212:95//Hs.98067:AA236822
- F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:
100:89//Hs.11469:U69567
- 10 F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:
339:60//Hs.129683:AF020761
- F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-
15 26:728:60//Hs.122967:AF059569
- F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682
- 20 F-PLACE1010134//H.sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889
- F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:
U41740
- 25 F-PLACE1010152
- F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792
- 30 F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582
- F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:
35 94//Hs.35225:H69637
- F-PLACE1010231
- 40 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:
97//Hs.27349:AB007917
- F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590
- 45 F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:
AI201540
- 50 F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813
- F-PLACE1010310//HOMEBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:
L20433
- 55 F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248

EP 1 074 617 A2

F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659

5 F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117

F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855

10 F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648

F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986

15 F-PLACE1010401

F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61//Hs.125257:
20 U70824

F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:
25 702:99//Hs.13313:AF039081

F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500

F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100

30 F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA,
complete cds//1.0:175:64//Hs.159273:AF054177

35 F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472

F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979

40 F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148

F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE
45 C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661

F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p
(PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186

50 F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394

F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858

55 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:
61//Hs.106387:AF029778

EP 1 074 617 A2

F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//0.012:258:62//Hs.144375:AA484200

5 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461

F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225

10 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102

F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076

15

F-PLACE1010662

20 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.37138:U35376

F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027

25 F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:96//Hs.50758:AF092564

30 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:AJ131244

35 F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391

F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284

40 F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]//6.0e-45:251:94//Hs.11379:AA594140

F-PLACE1010786

45

F-PLACE1010800

F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157

50

F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085

55 F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1 [H.sapiens]//2.9e-28:245:79//Hs.132736:AA583494

F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048

EP 1 074 617 A2

F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel.
[H.sapiens]//5.8e-67:336:97//Hs.130135:AA905493

5 F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244

F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:
10 98//Hs.118087:AB011182

F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671

15 F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:
65//Hs.1050:M85169

F-PLACE1010900

20 F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981

F-PLACE1010917

25 F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537

F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:
30 98//Hs.74750:AB011126

F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437:
35 98//Hs.66392:AF064244

F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985

F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154

40 F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444:59//Hs.585:X04506

F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632

45 F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721

F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931

50 F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032

F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:
55 179:67//Hs.1177:U10886

F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE

EP 1 074 617 A2

PHOSPHODIESTERASE BETA 2//6.2e-11:207:68//Hs.994:M95678

5 F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-35:310:
78//Hs.2407:Z49194

10 F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA,
complete cds//0.74:228:61//Hs.153640:U56998

F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320

15 F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663

F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037

20 F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317

F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370857

25 F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949

F-PLACE1011160

30 F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443

F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114

35 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase
mRNA, complete cds//6.9e-124:576:99//Hs.159140:AF038664

40 F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7e-101:469:99//Hs.8241:
AA283057

F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEESL70F
[C.elegans]//2.6e-62:221:88//Hs.101821:W27452

45 F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751

50 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4e-147:675:
99//Hs.23168:AB011101

F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:
98//Hs.15144:AC005014

55 F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803

F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191:

EP 1 074 617 A2

65//Hs.140950:AF070637

- 5 F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915
- F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160
- 10 F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310
- F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:99//Hs.5819:AF102265
- 15 F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs.159897:AB007970
- F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535
- 20 F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Raw3 [R.norvegicus]//6.7e-68:325:99//Hs.107245:AA627053
- 25 F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868
- F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552
- 30 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801:AB011102
- F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557:72//Hs.23094:M19503
- 35 F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:AI025204
- 40 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703:99//Hs.111138:AB018255
- F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482
- 45 F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264
- 50 F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997
- F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319
- 55 F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476
- F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:

EP 1 074 617 A2

84//Hs.153563:AF011333

5 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180

10 F-PLACE1011586//Homo sapiens hLRpl05 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462

F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778

15 F-PLACE1011641

20 F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631

F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661

25 F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086

F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745

30 F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234

35 F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366

F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350

40 F-PLACE1011725

F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853

45 F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891

F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240

50 F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693

F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660

55 F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664

EP 1 074 617 A2

F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775

5 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152

F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913

10 F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:AI357868

F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817

15 F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:AF059617

20 F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763

F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514

25 F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591

F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514

30 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756:AB018256

35 F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs.92381:AB007956

F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503

40 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330

F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627

45 F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831

F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627

50 F-PLACE2000017

F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557

55 F-PLACE2000030

EP 1 074 617 A2

- F-PLACE2000033//Human. adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512
- 5 F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.94653:AB011179
- F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59//Hs.79706:U53204
- 10
- F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128
- F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966
- 15
- F-PLACE2000061
- F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:662:86//Hs.23759:M98457
- 20
- F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:AF027219
- 25
- F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333
- F-PLACE2000100
- 30
- F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219
- F-PLACE2000111//H.sapiens mRNA for l-acylglycerol-3-phosphate O-acyltransferase//0.76:215:65//Hs.6587:U56417
- 35
- F-PLACE2000115
- 40
- F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:79//Hs.153014:AB002353
- F-PLACE2000132
- 45
- F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:AA718911
- 50
- F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U54645
- F-PLACE2000164
- 55
- F-PLACE2000170

EP 1 074 617 A2

F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179

F-PLACE2000176

F-PLACE2000187

F-PLACE2000216

F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933

F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:63//Hs.21560:AB002296

F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338

F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:AB007958

F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522

F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560

F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869

F-PLACE2000317

F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:M89796

F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088

F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299

F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817

F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645

F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045

F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861

F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032

EP 1 074 617 A2

F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638

5 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.158095:AB007953

F-PLACE2000398

10 F-PLACE2000399

F-PLACE2000404

15 F-PLACE2000411

F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080

20 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966

F-PLACE2000427

25 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719

F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257

30 F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2)//1.9e-20:418:64//Hs.130181:X85019

35 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080

40 F-PLACE2000455//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.0e-05:100:73//Hs.104239:AA488082

F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241

45 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381

F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080

50 F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262 ,

55 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384

EP 1 074 617 A2

- 5 F-PLACE3000020//Prostaglandin 12 (prostacyclin) receptor (IP)//0.00081:500:61//Hs.393:
D38128
- F-PLACE3000029
- 10 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248
- F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842
- 15 F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete
cds//1.0:186:62//Hs.122752:AF026445
- F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:
83//Hs.23711:AB018295
- 20 F-PLACE3000121
- F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081
- 25 F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:
59//Hs.6168:AB014603
- 30 F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243
- F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016
- 35 F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871
- F-PLACE3000148
- 40 F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:
99//Hs.6336:AB014572
- F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023
- 45 F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:
320:60//Hs.96253:U79666
- 50 F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:
88//Hs.153468:AB011147
- F-PLACE3000160
- 55 F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:
AF088219

EP 1 074 617 A2

F-PLACE3000194

5 F-PLACE3000197

F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546

10 F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975

F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN
 PRECURSOR//1.0:271:61//Hs.77522:X62744

15 F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216

F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377

20 F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA,
 complete cds//9.2e-56:200:85//Hs.133089:AF064019

25 F-PLACE3000226

F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568

30 F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4.
 Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced
 Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,
 6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker

35 DXS8032//1.2e-54:434:80//Hs.4943:Z98046

F-PLACE3000244

40 F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858

F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650

45 F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944

F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770

50 F-PLACE3000310

F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586

55 F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:
 AF088219

EP 1 074 617 A2

F-PLACE3000331

5 F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:AB014545

F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741

10 F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355

15 F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194

F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:234:63//Hs.7498:U41514

20 F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441

F-PLACE3000363

25 F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928

F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641

30 F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432

F-PLACE3000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73919:X81637

35 F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785

F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270

40 F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715

F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541

45 F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:116:78//Hs.77579:AF013263

50 F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:H61502

55 F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:AB018344

F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161

EP 1 074 617 A2

- 5 F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:183:93//Hs.108326:AB006202
- F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874
- 10 F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888
- F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190
- 15 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:AB018352
- 20 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:AC004131
- F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533
- 25 F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.40993:AF000148
- 30 F-PLACE4000063
- F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713
- 35 F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819
- F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058
- 40 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:AB007931
- 45 F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751
- F-PLACE4000129
- 50 F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627
- F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856
- 55 F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367
- F-PLACE4000192

EP 1 074 617 A2

F-PLACE4000211

5 F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594

F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329

10 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317

F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250

15 F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609

20 F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886

F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200

25 F-PLACE4000261

F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645

30 F-PLACE4000270

35 F-PLACE4000300

F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966

40 F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365

45 F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292

50 F-PLACE4000367

F-PLACE4000369

55 F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256

F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823

EP 1 074 617 A2

F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046

5 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026:AB014540

10 F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:AI275982

15 F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263:92//Hs.2397:Z70200

F-PLACE4000445

20 F-PLACE4000450

F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874

25 F-PLACE4000487//Sialophorin (gpL115, leukosialin, CD43)//3.0e-14:189:71//Hs.80738:X52075

F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951

30 F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289

F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731

35 F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022

40 F-PLACE4000548

F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.0035:510:59//Hs.39163:AF000986

45 F-PLACE4000581

50 F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:AI034080

F-PLACE4000593//ESTs, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239:79//Hs.109084:AI004675

55 F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074

F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.5e-47:

EP 1 074 617 A2

562:69//Hs.129685:AB002446

F-PLACE4000650

F-PLACE4000654

F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132

F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05299

F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG
50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.118634:U66688

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-148:706:
98//Hs.109299:AB014554

F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:M23254

F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877

F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:
AB002313

F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-35:299:
81//Hs.2407:Z49194

F-THYRO1000034

F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099

F-THYRO1000040//ESTs//0.30:331:59//Hs.87176:AI148326

F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:
63//Hs.101996:AB002345

F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//Hs.6654:
AB014557

F-THYRO1000085

F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065

F-THYRO1000107

F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8e-106:690:
86//Hs.23094:M19503

EP 1 074 617 A2

F-THYRO1000121

5 F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//Hs.103502:
U70732

10 F-THYRO1000129//Homo sapiens TED protein (TED).mRNA, complete cds//2.8e-155:732:
98//Hs.87619:AF087142

F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203

15 F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416

20 F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs.155464:
AF088219

F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-
05:261:61//Hs.152936:D63475

25 F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:
87//Hs.101238:Y11312

30 F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270

F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883

35 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:
99//Hs.43445:AJ005698

40 F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:
84//Hs.79672:AB014552

F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848

45 F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:U79297

F-THYRO1000241//EST//0.48:102:69//Hs.160764:AI313322

50 F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M27878

F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:
64//Hs.60103:AB014590

55 F-THYRO1000270

F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500

EP 1 074 617 A2

- F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068
- 5 F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C.elegans]//7.6e-92:431:99//Hs.122719:AA777803
- 10 F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.80731:M63175
- F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs.12002:AB018333
- 15 F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//6.9e-34:177:84//Hs.7833:U29091
- 20 F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919
- F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs.118401:AB011134
- 25 F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855
- F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.elegans]//5.8e-39:245:91//Hs.119095:T79413
- 30 F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572
- 35 F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238
- F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773
- 40 F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs.155024:U00115
- 45 F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X52520
- F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-22:248:76//Hs.162011:AA513663
- 50 F-THYRO1000488
- F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200
- 55 F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298
- F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120

EP 1 074 617 A2

- F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877
- 5 F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61//Hs.100058:AB006713
- 10 F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949
- F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs.151411:AF075587
- 15 F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322
- F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331
- 20 F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2685:Z50053
- F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081
- 25 F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941
- F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125
- 30 F-THYRO1000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267
- 35 F-THYRO1000662
- F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157
- 40 F-THYRO1000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//5.7e-49:281:77//Hs.116007:S79267
- F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46:368:57//Hs.26557:AA480380
- 45 F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452
- 50 F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324
- F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59//Hs.79706:U53204
- 55 F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085
- F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:

EP 1 074 617 A2

74//Hs.7977:AB007871

5 F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:AF061573

10 F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481

F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084

15 F-THYRO1000787

F-THYRO1000793

20 F-THYRO1000796

F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.4e-36:561:68//Hs.129685:AB002446

25 F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087

30 F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339

F-THYRO1000843

35 F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788

F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170

40 F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103

45 F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531

F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.92381:AB007956

50 F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529

55 F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836

F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:

EP 1 074 617 A2

56//Hs.112432:AC005263

5 F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:
D86963

10 F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase
(SUV3) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.7e-15:123:
90//Hs.106469:AF042169

F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907

15 F-THYRO1000983

F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646

20 F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307

F-THYRO1001003

25 F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369

F-THYRO1001033//H.sapiens mRNA for cyclin II//0.0061:287:60//Hs.3232:Z46788

30 F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:
79//Hs.51048:X68830

35 F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:
72//Hs.153014:AB002353

40 F-THYRO1001100//Human DNA-binding protein mRNA, 3'end//2.1e-74:741:74//Hs.159249:
Z99130

F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:
62//Hs.124024:AF053700

45 F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416

F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425

50 F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074

F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788

55 F-THYRO1001173

F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385

EP 1 074 617 A2

- F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163
- 5 F-THYRO1001204
- F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219
- 10 F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461
- F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:AJ002309
- 15 F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156
- 20 F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836
- F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182
- 25 F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872
- F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68//Hs.153563:AF011333
- 30 F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545
- 35 F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207
- F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939
- 40 F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79//Hs.12385:AB007877
- F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4e-157:740:97//Hs.138488:AB014607
- 45 F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993
- 50 F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946
- F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694
- 55 F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62//Hs.477:U05659

EP 1 074 617 A2

F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788

5 F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking
sequence//4.6e-33:153:81//Hs.102877:U41315

F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099

10 F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71//Hs.44782:
Z82215

15 F-THYRO1001480//SLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:
78//Hs.51048:X68830

F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943

20 F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904

F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663

25 F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211

F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046

30 F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335

35 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:
95//Hs.25306:AF070572

F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27655

40 F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs.75551:
L12535

F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849

45 F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071

F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046

50 F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2e-13:108:
86//Hs.141045:AA191659

55 F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:
540:55//Hs.95958:M91463

F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568

EP 1 074 617 A2

- 5 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089
- F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF010238
- 10 F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.122908:AF070552
- F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691
- 15 F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//2.5e-51:296:92//Hs.3826:U69560
- F-THYRO100173 8//EST//6.9e-30:180:94//Hs.58641:W81229
- 20 F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813
- F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590
- 25 F-THYRO1001772//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725
- 30 F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324
- F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//Hs.11711:AB002295
- 35 F-THYRO1001828
- F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823
- 40 F-THYRO1001895//Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288:65//Hs.51061:M24283
- 45 F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198
- F-VESEN1000122
- 50 F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885
- F-Y79AA1000033
- 55 F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:230:66//Hs.431:L13689

EP 1 074 617 A2

F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:U78521

5 F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680

F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053

10 F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0022:684:58//Hs.83190:U29344

F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860

15

F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.9242:AF081192

20 F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079

F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623

25 F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134

30 F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365

F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919

35

F-Y79AA1000328

40 F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:AF071309

F-Y79AA1000346

45 F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853

F-Y79AA1000355

50

F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908

F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897

55

F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219

EP 1 074 617 A2

- F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018
- 5 F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete
cds//0.0047:315:66//Hs.26285:AF082516
- F-Y79AA1000480
- 10 F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871
- F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521
- 15 F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:
AF053356
- 20 F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:
371:63//Hs.8991:AF068706
- F-Y79AA1000574//Human mRNA for GC box bindig protein, complete cds//0.95:258:
25 62//Hs.150557:D31716
- F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:
755:97//Hs.21811:AF091080
- 30 F-Y79AA10006277//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-
136:644:98//Hs.60580:AF060503
- 35 F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:
AF006513
- F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete
40 cds//1.6e-181:850:98//Hs.83023:AF093670
- F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969
- 45 F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377
- F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067
- 50 F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468
- F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:
97//Hs.5151:AF098799
- 55 F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231

EP 1 074 617 A2

- F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085
- 5 F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:AF059569
- F-Y79AA1000805
- 10 F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568
- F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0048:630:57//Hs.83190:U29344
- 15 F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956
- 20 F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368:99//Hs.86660:AA398644
- F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288:D16815
- 25 F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699
- 30 F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//6.9e-69:310:94//Hs.76822:AI359536
- F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270
- 35 F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M23892
- 40 F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204
- F-Y79AA1001023
- 45 F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
- 50 F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590
- F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381
- 55 F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511

EP 1 074 617 A2

F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047

F-Y79AA1001078

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F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.55967:AF022654

10

F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381

F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293

15

F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248

F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646

20

F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965

F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054

25

F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436

F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879

30

F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892

35

F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240

40

F-Y79AA1001299//Human Ini1 mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847

F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395

45

F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555

F-Y79AA1001384

50

F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599

F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424:96//Hs.154221:H23167

55

F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489

EP 1 074 617 A2

F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683

F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465

5

F-Y79AA1001533//ESTs; Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Homo sapiens]//0.95:256:63//Hs.29974:AI360447

10

F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744

F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659

15

F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851

F-Y79AA1001581//Cyclin-dependept kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398

20

F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783

F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109

25

F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426

30

F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:AB014583

F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421:94//Hs.107039:W27244

35

F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385

40

F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:X04526

45

F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302

F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877

50

F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191

55

F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:AI018620

F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//Hs.113082:AB007903

EP 1 074 617 A2

F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079

5 F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein
[H.sapiens]//2.9e-62:313:98//Hs.15709:W81213

F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533

10

F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142:
90//Hs.103349:AI141124

15 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:
67//Hs.104115:X52332

20 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:
62//Hs.106387:AF029778

F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173

25 F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete
cds//0.98:430:58//Hs.78501:L13720

F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382

30

F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611

F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943

35

F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348:
88//Hs.18122:AI338045

40 F-Y79AA1002093

F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865

45

F-Y79AA1002115

F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395

50

F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165:90//Hs.6473:
AA853955

55 F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393:
62//Hs.77864:AB014538

F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515

EP 1 074 617 A2

- 5 F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldotenax]/2.3e-113:568:96//Hs.111637:AA305890
- F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]/8.6e-33:338:73//Hs.26662:U55984
- 10 F-Y79AA1002211//ESTs/2.6e-15:121:75//Hs.159584:AA524477
- F-Y79AA1002220//EST/0.010:360:60//Hs.136341:AA482508
- 15 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds/0.0041:203:63//Hs.1560:D42045
- F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds/4.1e-176:821:98//Hs.100729:AB014592
- 20 F-Y79AA1002246//Human involucrin mRNA/5.6e-05:525:59//Hs.157091:M13903
- F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds/2.2e-160:748:98//Hs.96731:AB014555
- 25 F-Y79AA1002298//ESTs/2.5e-05:115:77//Hs.87164:T84489
- 30 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds/2.1e-130:622:97//Hs.30898:AB014534
- F-Y79AA1002311//ESTs/4.9e-19:126:94//Hs.58595:AA830999
- 35 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds/0.028:587:58//Hs.2363:L36069
- 40 F-Y79AA1002361//ESTs/8.7e-29:149:100//Hs.156074:AA824377
- F-Y79AA1002399
- 45 F-Y79AA1002407//ESTs/1.5e-25:183:89//Hs.110031:T52569
- F-Y79AA1002416//CTP synthetase/9.1e-51:489:72//Hs.84112:X52142
- 50 F-Y79AA1002431
- F-Y79AA1002433//EST/0.0037:94:71//Hs.136780:AA772318
- 55 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152/1.1e-37:263:69//Hs.55452:AC003973

EP 1 074 617 A2

F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765

5 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302

Homology Search Result Data 5.

10

The result of the homology search of the Human Unigene using the clone sequence of 3'-end.
Data include

15

the name of clone,

title of the top hit data,

20

the P-value: the length of the compared sequence: identity (%), and

the Accession No. of the top hit data, as in the order separated by //.

25

Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

Data are not shown for the clones in which the P-value was higher than 1.

30

R-HEMBA1000005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME III [Caenorhabditis elegans]//5.6e-93:501:93//Hs.13015:AA628434

35

R-HEMBA1000030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233

40

R-HEMBA1000042//Archain//1.4e-45:282:89//Hs.33642:X81198

R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:72//Hs.154326:D42087

45

R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243340

R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329

50

R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788

R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]//4.4e-90:502:90//Hs.55918:AA151667

55

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514:94//Hs.27197:AB018340

EP 1 074 617 A2

R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435:77//Hs.153026:AB014540

5 R-nnnnnnnnnnnn//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//7.7e-92:428:100//Hs.126925:AA931237

10 R-HEMBA1000158

R-nnnnnnnnnnnn//ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58:91//Hs.5570:AI377863

15 R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545

R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366

20 R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927

R-HEMBA1000201//Human Ini1 mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847

25 R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311

R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532

30 R-nnnnnnnnnnnn//EST//2.2e-100:498:96//Hs.161570:W80404

R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70//Hs.127649:AB007874

35 R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276:75//Hs.5737:AB007944

40 R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019

R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808

45 R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424

R-nnnnnnnnnnnn//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.9e-14:208:73//Hs.93332:AA811920

50 R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485

55 R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962

R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409

EP 1 074 617 A2

- 5 R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122:67//Hs.129748:AB011099
- R-nnnnnnnnnnnn//ESTs//7.4e-76:386:97//Hs.22276:AA191323
- 10 R-nnnnnnnnnnnn//Human Ca²⁺-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160:98//Hs.151301:U36448
- R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e-103:489:99//Hs.108881:AI018024
- 15 R-nnnnnnnnnnnn//ESTs//9.3e-99:472:98//Hs.163512:AA903238
- R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560
- 20 R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//Hs.73614:U83460
- 25 R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243
- R-HEMBA1000357//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:K00629
- 30 R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857
- R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938
- 35 R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960
- 40 R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//Hs.73614:U83460
- 45 R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878
- R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:AI340248
- 50 R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]//1.1e-44:447:75//Hs.42849:N31920
- 55 R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//6.1e-92:373:99//Hs.48675:AI005282
- R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700

EP 1 074 617 A2

- R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140
- 5 R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:
AJ001189
- 10 R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143
- R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014
- 15 R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349
- R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316
- 20 R-HEMBA1000460
- R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370
- 25 R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155464:
AF088219
- 30 R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to
Drosophila melanogaster ring canel protein. [H.sapiens]//1.1e-31:181:94//Hs.61454:
AA312449
- R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528
- 35 R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087
- R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571
- 40 R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318
- R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531
- 45 R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885
- R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414
- 50 R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280
- 55 R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:
92//Hs.155510:U15782
- R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1
[H.sapiens]//1.3e-117:550:99//Hs.99722:AI422277

EP 1 074 617 A2

- R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809
- 5 R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317
- R-nnnnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699
- 10 R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881
- R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:W74481
- 15 R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196
- R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128
- 20 R-nnnnnnnnnnnnn
- R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788
- 25 R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944
- R-HEMBA1000591//Homo sapiens mRNA for EIB-55kDa-associated protein//3.9e-113:591:94//Hs.155218:AJ007509
- 30 R-HEMBA1000592//TYROSINE-PROTEIN KINASE
- 35 ITK/TSK//0.024:309:61//Hs.89519:L10717
- R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041
- 40 R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.158334:U86136
- R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424
- 45 R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438
- R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:AA643235
- 50 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:AB014590
- 55 R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:

EP 1 074 617 A2

AB002390

- 5 R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929
- R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136
- 10 R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922
- R-HEMBA1000682//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403
- 15 R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:AI141736
- R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:AF057280
- 20 R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672
- 25 R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213
- R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/isomerases [C.elegans]//7.2e-113:572:95//Hs.28644:AI018612
- 30 R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449:75//Hs.74478:U33931
- 35 R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777
- R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110
- 40 R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs.155464:AF088219
- R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131
- 45 R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309:75//Hs.10458:AF088219
- 50 R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612
- R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//1.3e-48:284:90//Hs.103458:X53795
- 55 R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:

EP 1 074 617 A2

87//Hs.154326:D42087

5 R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939

R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027

10 R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977

15 R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410:77//Hs.154103:AF061258

R-HEMBA1000851

20 R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284:80//Hs.159608:U46689

R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:AI265794

25 R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202

R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608

30 R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951

35 R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219

R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:AI203154

40 R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672

R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508

45 R-HEMBA1000919

R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597

50 R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619

R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:AB018291

55 R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074

R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:

EP 1 074 617 A2

81//Hs.5247:AF029750

5 R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0508//6.8e-51:362:84//Hs.159187:AB007977

R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:AI363498

10 R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.44766:
AJ007590

R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:AI018170

15

R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878

R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.14 7434:AI214464

20

R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902

R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:AI281881

25

R-HEMBA1001007

R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764

30

R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein
[H.sapiens]//2.6e-58:280:100//Hs.128738:AA970836

35 R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587:
95//Hs.158287:AB007937

40 R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:95//Hs.58393:
X05360

R-HEMBA1001020//ESTs//0.52:86:72//Hs.69683:AA115292

45

R-HEMBA1001022//ESTs//3.4e-18:102:100//Hs.63243:AI123912

R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336

50

R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:AI345543

R-nnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616

55

R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:
79//Hs.132942:AB014521

EP 1 074 617 A2

R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886

R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813

5

R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X14420

10

R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0492//2.7e-21:417:64//Hs.127338:AB007961

R-HEMBA1001080

15

R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788

R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674

20

R-HEMBA1001094

R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245

25

R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs.155464:
AF088219

30

R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974

R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320

35

R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:
M15530

R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341

40

R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265

45

R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs.155464:
AF088219

50

R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//1.1e-39:309:82//Hs.96337:AA225358

55

R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:
238:60//Hs.127338:AB007961

R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896

R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5
[H.sapiens]//0.27:305:62//Hs.100238:U69194

EP 1 074 617 A2

R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080
 5
 R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316
 R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932
 10
 R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728
 R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435
 15
 R-nnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181
 20
 R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674
 R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534
 25
 R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324
 R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219
 30
 R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162
 35
 R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214
 R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019
 40
 R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977
 R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950
 45
 R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [S.cerevisiae]//1.3e-77:458:92//Hs.9398:N41838
 50
 R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259
 R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080
 55
 R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816

EP 1 074 617 A2

R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837

5 R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334

R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550

10 R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458

R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482

15 R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439

R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204

20 R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081

R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714

25 R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364

R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

30 R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199

R-HEMBA1001415

35 R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82//Hs.42674:U61981

R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704

40 R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263

R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982

45 R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546

R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077

50 R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304:88//Hs.23094:M19503

55 R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220

R-HEMBA1001463

EP 1 074 617 A2

R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66//Hs.36232:D80008

5 R-HEMBA1001478

R-HEMBA1001497

10 R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426

R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528:84//Hs.23094:M19503

15

R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269

R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA-702493

20

R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723

R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270

25

R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348

30 R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs.155464:AF088219

R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324

35

R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880

40

R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030

R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652

45

R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329

R-HEMBA1001589

50

R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431:88//Hs.26625:W25874

55

R-HEMBA1001608//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.3e-73:533:82//Hs.103948:K00627

EP 1 074 617 A2

R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]//4.5e-93:537:90//Hs.20218:AA628530

5 R-nnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362:60//Hs.132206:AF039694

R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158

10

R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623

15 R-nnnnnnnnnnnn//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442:95//Hs.63888:AA203398

R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554

20 R-HEMBA1001658

R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:AF029343

25

R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943

30 R-HEMBA1001675

R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962

35

R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424

R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916

40

R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:AB014598

45

R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960

R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095

50

R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//1.8e-46:236:98//Hs.132948:AA194452

55

R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs.155464:AF088219

R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS

EP 1 074 617 A2

CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105

5 R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712

R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353

10

R-HEMBA1001744

R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623

15

R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162

R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145

20

R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306

R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721

25

R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053

R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243

30

R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823

R-nnnnnnnnnnnn//Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180:AF039019

35

R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//9.0e-114:548:98//Hs.118164:AB007969

40

R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334

R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179

45

R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07290

R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707

50

R-nnnnnnnnnnnn//ESTs//2.2e-101:480:99//Hs.159940:AA971578

R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210

55

R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250

EP 1 074 617 A2

R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513

R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446

5 R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.1e-109:553:96//Hs.78946:AB014517

10 R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853

R-HEMBA1001866//Myelin oligodendrocyte glycoprotein {alternative products}//1.9e-37:357:76//Hs.53217:Z48051

15 R-nnnnnnnnnnnn//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//2.3e-32:193:94//Hs.9489:R84329

20 R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969

R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128

25 R-HEMBA1001910

R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.5e-73:347:100//Hs.30991:AA994438

30 R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//5.1e-57:320:91//Hs.91251:U66685

35 R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706

R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125

40 R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145

R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-99:482:98//Hs.96849:AA879470

45 R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390

50 R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668

R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452

55 R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866

EP 1 074 617 A2

R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421

R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048

R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825

R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178

R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932

R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717

R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353

R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6e-91:448:97//Hs.5687:AJ005801

R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930

R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837

R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550

R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538

R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312

R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-51:254:85//Hs.15731:AB011135

R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764

R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996

R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354

R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124:AF019369

R-HEMBA1002113//Prostaglandin 12 (prostacyclin) synthase //1.4e-76:280:90//Hs.61333:D83402

EP 1 074 617 A2

- R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence//1.4e-87:362:94//Hs.103443:AF065854
- 5 R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:AI357868
- 10 R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X83957
- R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734
- 15 R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199
- R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642
- 20 R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337
- R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:AF023674
- 25 R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915
- 30 R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043
- R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081
- 35 R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457
- R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622
- 40 R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:AB007958
- 45 R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357
- R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503
- 50 R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342
- R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315
- 55 R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151

EP 1 074 617 A2

R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:AB014606

5 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//Hs.25664:AF089814

10 R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202

R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426

15 R-HEMBA1002257

R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675

20 R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314

R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595

25 R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818

R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679

30 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:AB018314

35 R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822

R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094

40 R-nnnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:661:93//Hs.119023:AF092563

R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435

45 R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237

R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954

50 R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-87:429:96//Hs.13209:AI417849

55 R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238AA476267

R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:

EP 1 074 617 A2

D38522

- 5 R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069
- R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085
- 10 R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395
- R-nnnnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:488:95//Hs.108115:AA582193
- 15 R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80//Hs.43681:AL022394
- 20 R-HEMBA-1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs.155464:AF088219
- R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:AI188995
- 25 R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133
- R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449
- 30 R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990
- R-nnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:AJ011972
- 35 R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715
- 40 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564:93//Hs.129928:AB007923
- R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700
- 45 R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804
- R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:AI281881
- 50 R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012
- R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs.32567:AF073519
- 55 R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs.155464:AF088219

EP 1 074 617 A2

R-nnnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587:97//Hs.151411:AF075587

5 R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904

R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838

10 R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055

R-HEMBA1002621

15 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380:97//Hs.91338:AB018351

20 R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881

R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715

25 R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041

R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970

30 R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406:81//Hs.108966:U48696

R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:AB018307

35 R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945

40 R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-104:560:92//Hs.161748:T64896

R-nnnnnnnnnnnnn//EST//0.15:136:69//Hs.129570:AA995396

45 R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282

50 R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477

R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302:86//Hs.15519:AB018315

55 R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884

EP 1 074 617 A2

R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:AB014521

5 R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168

R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163

10 R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526

R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:AI375792

15 R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090

R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545:95//Hs.74750:AB011126

20

R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127

R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491

25

R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58//Hs.48824:D87717

30 R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75//Hs.153563:AF011333

R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709

35

R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320

R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116:559:97//Hs.28307:AF071185

40

R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//Hs.79706:U53204

45

R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013

R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25:137:98//Hs.5337:AA243757

50

R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514

55

R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830

R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827

EP 1 074 617 A2

- R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670
- 5 R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//Hs.33787:AF037261
- 10 R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011
- R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820
- 15 R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087
- 20 R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481
- R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165
- 25 R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679
- R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732
- 30 R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:AI190892
- R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085
- 35 R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369
- R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI000405
- 40 R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579
- 45 R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219
- R-nnnnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064
- 50 R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113:560:96//Hs.125749:AI377682
- R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:290:85//Hs.113283:AF018080
- 55 R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480

EP 1 074 617 A2

R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577

R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827

R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366

R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN
KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:
79//Hs.114905:AA088442

R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA,
complete cds//1.3e-119:578:97//Hs.44097:AF054182

R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627

R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238

R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903

R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:
99//Hs.14146:W92235

R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402

R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249

R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:
AF088219

R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223

R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds
[M.musculus]//4.2e-100:531:94//Hs.104800:AA709155

R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624

R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058

R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete
cds//2.1e-13:109:88//Hs.118717:U86751

R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:AI370845

R-HEMBA1003136//ESTs, Weakly similar to MANNOSE-1-PHOSPHATE
GUANYLTRANSFERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615

EP 1 074 617 A2

R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219

5 R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670

10 R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933

R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389

15 R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000

R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804

20 R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:AB014540

25 R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943

R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265

30 R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817

35 R-HEMBA1003227//ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294:W27666

R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305

40 R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834

R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.152663:AF068864

45 R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929

50 R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219

R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392

55 R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785

R-HEMBA1003281

EP 1 074 617 A2

R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109

5 R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266

R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353

10 R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504

R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872

15 R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869

20 R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119

25 R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173

R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:AF026029

30 R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357

35 R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540

R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651

40 R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588

R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247

45 R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-11:261:65//Hs.87578:AI125363

R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847

50 R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127

R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204

55 R-nnnnnnnnnnnnn//ESTs//1.7e-24:188:85//Hs.70266:Z78309

R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563

EP 1 074 617 A2

- R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013
- 5 R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696
- R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121
- 10 R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516
- R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080
- 15 R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688
- R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760
- 20 R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058
- R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817
- 25 R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673
- R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs.91619:AA552351
- 30 R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734
- 35 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522
- R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058
- 40 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.58598:AA625440
- R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099
- 45 R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892
- 50 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065
- R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212
- 55 R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087

EP 1 074 617 A2

R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042

5 R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374

R-HEMBA1003615

10 R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167

R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387

15 R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888

R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021

20 R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!
[H.sapiens]//9.3e-24:189:84//Hs.142208:AA209438

R-HEMBA1003640//SLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:
25 81//Hs.51048:X68830

R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010

30 R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783

R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0488//5.6e-44:245:77//Hs.67619:AB007957

35 R-HEMBA1003662//Human TBX2 (TXB2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:
U28049

40 R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635

R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2
[H.sapiens]//4.1e-87:434:97//Hs.9489:R84329

45 R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:
61//Hs.72925:M91083

50 R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-
101:528:95//Hs.22934:AA581379

R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916

55 R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:
80//Hs.110194:M29873

EP 1 074 617 A2

R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064

5 R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1
 PRECURSOR//0.94:367:62//Hs.1139:X77777

10 R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:
 85//Hs.113283:AF018080

15 R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TASK) mRNA,
 complete cds//1.2e-33:377:74//Hs.24040:AF006823

R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847

20 R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839

R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592

25 R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:
 96//Hs.11282:AI147040

R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247

30 R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089

35 R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR
 BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214

R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:
 93//Hs.18171:AA524327

40 R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600

R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236

45 R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:
 100//Hs.107747:AI357868

50 R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295

R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344

55 R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163

R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:
 AF088219

EP 1 074 617 A2

5 R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE
CHAIN 2 [Paramecium tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333

R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161

10 R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033

R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547

15 R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A
CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911

R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:
79//Hs.61408:AF070621

20 R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930

R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF068179

25 R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788

R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187

30 R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659

R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276:
81//Hs.72660:AB011157

35 R-HEMBA1003939

40 R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669

R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545

45 R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591

R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562

50 R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253

R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525

55 R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882

R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!

EP 1 074 617 A2

[H.sapiens]//2.2e-91:448:97//Hs.117834:AA766771

R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756

5

R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:81//Hs.150275:D87682

10

R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105

R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899

15

R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011

R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774

20

R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461

R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191

25

R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253

R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens]//1.5e-22:365:70//Hs.99692:AA811804

30

R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469

R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M11717

35

R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754

R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080

40

R-HEMBA1004074//EST//1.0:152:61//Hs.149093:AI243988

45

R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652

R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251

50

R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:D50918

R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562

55

R-HEMBA1004133

EP 1 074 617 A2

R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736

R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320

5 R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs.155464:AF088219

10 R-HEMBA1004150//GRANALCALCIN//0.99:357:59//Hs.79381:M81637

R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087

15 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96//Hs.59988:AF067855

20 R-HEMBA1004199

R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701

25 R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552:94//Hs.10092:AI189282

R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:AB014518

30 R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748

35 R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617

R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.0e-16:117:91//Hs.92033:AA255832

40 R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353

45 R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389

R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258

50 R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221:86//Hs.7089:W37284

55 R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962

R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!

EP 1 074 617 A2

[H.sapiens]/1.4e-89:465:95//Hs.113660:D20018

R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931

5

R-nnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:AF091081

10

R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]/4.4e-92:559:89//Hs.28298:AA203228

15

R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101766:AF022795

20

R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884:U13061

R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]/3.6e-93:496:94//Hs.14337:AA534961

25

R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426

R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679

30

R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199:X16281

R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904

35

R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714

R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561

40

R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231

R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336

45

R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240

R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:D89667

50

R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353

55

R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494

EP 1 074 617 A2

- R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869
- 5 R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057
- R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264
- 10 R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084
- R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219
- 15 R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717
- R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933
- 20 R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:AI123518
- 25 R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503
- R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829
- 30 R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033
- R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172
- 35 R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306
- 40 R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034
- R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941
- 45 R-HEMBA1004507
- R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271
- 50 R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:281:89//Hs.58414:AA196947
- 55 R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972

EP 1 074 617 A2

R-HEMBA1004554

5 R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924

R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913

10 R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243

R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769

15 R-nnnnnnnnnnnn//ESTs//6.0e-22:190:82//Hs.42530:N41661

R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767

20 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327:85//Hs.159897:AB007970

R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:AI375915

25 R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785

R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152

30 R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12263:AA282393

35 R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:AI278454

R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442

40 R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348

R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI057560

45 R-HEMBA1004672//EST//6.7-e-76:315:97//Hs.20821:R19368

R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI093252

50 R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562

R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA599042

55 R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:AI281881

R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs.155464:

EP 1 074 617 A2

AF088219

5 R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:AI309235

R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequencer//2.1e-44:467:73//Hs.91916:AF035317

10 R-HEMBA1004733//EST//0.99:84:65//Hs.161372:AI423151

R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275

15 R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//9.5e-39:296:82//Hs.51187:U82828

R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651

20 R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:AI279428

R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081

25 R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L06498

R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679

30 R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI049504

R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380

35 R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//1.4e-47:379:81//Hs.141273:H66705

40 R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092

R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633

45 R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476

R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167

50 R-nnnnnnnnnnnnn

R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732

55 R-HEMBA1004806

R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N47676

EP 1 074 617 A2

- R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI053784
- 5 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:M74002
- R-HEMBA1004847
- 10 R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120
- R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267
- 15 R-HEMBA1004864
- R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362
- 20 R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409
- R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676
- 25 R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:AI357470
- R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011
- 30 R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:89//Hs.40100:AB002390
- 35 R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388
- R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053
- 40 R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:80//Hs.1361:M55053
- R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:AI422883
- 45 R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215
- 50 R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434
- R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007
- 55 R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074
- R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040

EP 1 074 617 A2

- R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035
- 5 R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065
- R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404
- 10 R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.129734:AJ001683
- R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329
- 15 R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894
- 20 R-HEMBA1004995
- R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520
- 25 R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212
- 30 R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:AB014548
- R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-95:491:94//Hs.16085:AI261382
- 35 R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:85//Hs.22271:D26067
- 40 R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443:78//Hs.139019:N99348
- 45 R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542:87//Hs.16258:AI376436
- R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145
- 50 R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451
- R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.79385:U90905
- 55 R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789

EP 1 074 617 A2

- R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U17077
- 5 R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958
- R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545:96//Hs.11170:AF080561
- 10 R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739
- R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952
- 15 R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85//Hs.19949:X98173
- 20 R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394:75//Hs.67619:AB007957
- R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362:77//Hs.132206:AF039694
- 25 R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397
- 30 R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914
- R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766
- 35 R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239
- R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191:61//Hs.26931:AF061836
- 40 R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284
- R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687
- 45 R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W84331
- R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834
- 50 R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393896
- R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1e-49:277:93//Hs.72660:AB011157
- 55 R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA668862

EP 1 074 617 A2

R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391

5 R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611

R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750

10 R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs.155464:AF088219

15 R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519

R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046

20 R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169

R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472

25 R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606

R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI341467

30 R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.129735:AF010144

35 R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350

R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653

40 R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305

R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.54486:X54150

45 R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:489:92//Hs.43864:AA131568

50 R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278

R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725

55 R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059

R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757

EP 1 074 617 A2

R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:453:99//Hs.4854:AF041248

5 R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960

10 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//Hs.6445:L40391

R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961

15 R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494

20 R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353

R-HEMBA1005472//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//8.4e-73:464:87//Hs.103948:K00627

25 R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445

R-HEMBA1005497

30 R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788

35 R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//Hs.62608:S58544

R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870

40 R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//2.6e-82:387:99//Hs.67466:AI219740

R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322

45 R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045

50 R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981

R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788

55 R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//8.6e-115:578:95//Hs.17035:AI080471

R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350

EP 1 074 617 A2

R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926

5 R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627

R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:439:91//Hs.22897:R43193

10 R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:182:76//Hs.133526:N21103

15 R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709

R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497

20 R-HEMBA1005577

R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64//Hs.57929:AB011538

25 R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392

R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539

30 R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990

R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905

35 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820

R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA573125

40 R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390

R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422

45 R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//2.8e-95:539:92//Hs.19400:AA662845

50 R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5e-38:317:78//Hs.1721:X58377

R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:65//Hs.15245:AF041081

55 R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA731522

EP 1 074 617 A2

- R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234:80//Hs.10458:AF088219
- 5 R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973
- R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI279477
- 10 R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:322:88//Hs.82193:M13450
- 15 R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343:81//Hs.154103:AF061258
- R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235:64//Hs.159437:U44060
- 20 R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//1.7e-47:376:84//Hs.26988:U66406
- 25 R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055
- R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI159943
- 30 R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)//1.2e-45:398:79//Hs.155481:AJ006470
- 35 R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815
- R-nnnnnnnnnnnn//EST//0.098:125:68//Hs.136945:AA765672
- 40 R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096
- R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:U21936
- 45 R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974
- R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.10458:AF088219
- 50 R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:AI038601
- 55 R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960
- R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI039201

EP 1 074 617 A2

- R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI080618
- 5 R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911
- R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917
- 10 R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970
- R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:AI022252
- 15 R-HEMBA1005894
- R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:AI215686
- 20 R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI076363
- R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632
- 25 R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446:75//Hs.59403:AB011098
- R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867
- 30 R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:AI199418
- R-HEMBA1005963
- 35 R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.26285:AF082516
- 40 R-HEMBA1005991//Human antiseecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199
- R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:AI080618
- 45 R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:AI379875
- R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436
- 50 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268
- 55 R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951
- R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508

EP 1 074 617 A2

R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490

5 R-nnnnnnnnnnnnn

R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612

10 R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517

R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313

15 R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//Hs.73614:U83460

R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297

20 R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293

R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931

25 R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:AB007958

30 R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542

R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212

35 R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930

R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627

40 R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906

R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125

45 R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557

50 R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//Hs.23617:AA928683

55 R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522

EP 1 074 617 A2

R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:AF083384

5 R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881

10 R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]//1.2e-97:529:93//Hs.10552:AA524401

15 R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//2.7e-88:484:92//Hs.104129:AA923278

R-nnnnnnnnnnnn//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770

20 R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.cerevisiae]//1.6e-66:377:91//Hs.108674:W25821

R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735

25 R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019

R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037

30 R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:U33931

35 R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculus]//5.6e-76:417:94//Hs.111754:AI204587

40 R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219

R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184

45 R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204

50 R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:AI417075

R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382

55 R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008

R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787

EP 1 074 617 A2

- R-HEMBA1006377//EST//0.0097:145:621//Hs.133027:AI049830
- 5 R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:AB011166
- R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651
- 10 R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:5 82:84//Hs.23094:M19503
- 15 R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923
- R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778
- 20 R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878
- R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004
- 25 R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964
- R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380
- 30 R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033
- R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784
- 35 R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895
- 40 R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17:342:63//Hs.111730:AA604403
- R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441
- 45 R-HEMBA1006474
- R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984
- 50 R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701
- 55 R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223

EP 1 074 617 A2

R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350

R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720

R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387

R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117

R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505

R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566

R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300

R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628

R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934

R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331

R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154

R-HEMBA10065597//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594

R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064

R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876

R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725

R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876

R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280

R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390

R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219

R-HEMBA1006612

EP 1 074 617 A2

R-nnnnnnnnnnnn//ESTs//1.2e-25:225:80//Hs.138852:AA284247

R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630

5

R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067

10

R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!
[H.sapiens]//2.7e-91:426:100//Hs.139469:AI299889

15

R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186:100//Hs.109818:AA411185

R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777

20

R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:U40282

R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427

25

R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511

R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102

30

R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594

R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842

35

R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435

40

R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263

R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695

45

R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene
[H.sapiens]//1.1e-92:483:94//Hs.6525:AI205313

R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062

50

R-HEMBA1006717

R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002

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R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627

EP 1 074 617 A2

R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099

5 R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646

R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763

10 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881

R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562

15 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936

R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705

20 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978

R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333

25 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305

R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272

30 R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556

R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087

35 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665

40 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:AB018315

45 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453

R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739

50 R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117

R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400

55 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308

R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712

EP 1 074 617 A2

- R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382
- 5 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:AJ010841
- R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321
- 10 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457
- R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827
- 15 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325
- 20 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679
- R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440
- 25 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293
- R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:AI248363
- 30 R-HEMBA1007045
- R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788
- 35 R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839
- R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140
- 40 R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272
- R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866
- 45 R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//7.2e-40:163:83//Hs.152369:AA504818
- 50 R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087
- R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025
- 55 R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597
- R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:

EP 1 074 617 A2

D25272

5 R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438

R-HEMBA1007147

10 R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818

R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674

15 R-nnnnnnnnnnnnn//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085

R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954

20 R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051

R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987

25 R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990

30 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:AB018340

R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864

35 R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934

R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394

40 R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062

R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207

45 R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543

R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804

50 R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990

R-HEMBA1007301

55 R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917

EP 1 074 617 A2

R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]/5.5e-15:311:64//Hs.142764:AA205569

5 R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:K00629

10 R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.154069:U06452

R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848

15 R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684

20 R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333

R-HEMBA1007348//ESTs, Weakly similar to putative p150 [H.sapiens]/3.3e-44:341:71//Hs.111730:AA604403

25 R-HEMBA1007349//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090

30 R-HEMBA1007350//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969

R-HEMBA1007351//ESTs//7.5e-21:234:76//Hs.157049:AI345418

35 R-HEMBA1007352//ESTs//2.2e-36:371:78//Hs.56562:AA056332

R-HEMBA1007353//ESTs//3.2e-76:373:97//Hs.140190:AA701449

40 R-HEMBA1007354//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III [Caenorhabditis elegans]/6.0e-92:477:95//Hs.4877:AA418465

45 R-HEMBA1007355//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928

R-HEMBA1007356//ESTs//1.8e-43:361:71//Hs.108206:N64702

50 R-HEMBA1007357//EST//7.6e-70:367:95//Hs.140860:R42954

R-HEMBA1007358//EST//1.5e-45:262:91//Hs.157627:AI357802

55 R-HEMBA1007359//ESTs//0.039:91:74//Hs.163189:AA236903

R-HEMBA1007360//ESTs//3.0e-104:550:94//Hs.152395:AA533107

EP 1 074 617 A2

R-HEM BB1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUBUNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//Hs.116490:AA659584

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R-HEM BB1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939

10

R-HEM BB1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997

15

R-HEM BB1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353

20

R-HEM BB1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193

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R-HEM BB1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:AB014540

R-HEM BB1000113//EST//8.2e-94:437:100//Hs.136893:AA805239

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R-HEM BB1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521

R-HEM BB1000136//ESTs//0.043:262:59//Hs.61304:AA025692

35

R-HEM BB1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915

R-HEM BB1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951

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R-HEM BB1000173//EST//9.6e-44:258:76//Hs.161917:AA483223

R-HEM BB1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558

45

R-HEM BB1000198//ESTs//1.0:123:62//Hs.116602:AA665965

R-HEM BB1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353

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R-HEM BB1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364

R-HEM BB1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019

55

R-HEM BB10002267//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//5.1e-73:449:89//Hs.16803:AA843214

R-HEM BB1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106

EP 1 074 617 A2

R-HEM BB1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs.155464:AF088219

5 R-HEM BB1000250//EST//8.8e-12:284:64//Hs.145960:AI276783

R-HEM BB1000258//EST//4.5e-14:315:66//Hs.162551:AA584782

10 R-HEM BB1000264

R-HEM BB1000266//ESTs, Weakly similar to similar to the beta transducin family [C.elegans]//2.7e-102:556:93//Hs.16079:AA083522

15

R-HEM BB1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385

20 R-HEM BB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:AB011129

R-HEM BB1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458

25 R-HEM BB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353

R-HEM BB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601

30

R-HEM BB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034

35 R-HEM BB1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs.155464:AF088219

R-HEM BB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576

40 R-HEM BB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480

R-HEM BB-1000337//ESTs//2.1e-80:391:97//Hs.118990:AI378084

45 R-HEM BB1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs.155464:AF088219

R-HEM BB1000339//EST//5.8e-41:336:79//Hs.151873:AA205736

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R-HEM BB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651

R-HEM BB1000343//EST//1.1e-77:396:95//Hs.162664:AA605020

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R-HEM BB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008

EP 1 074 617 A2

R-HEM BB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA463590

5 R-HEM BB1000374//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0487//2.3e-56:335:77//Hs.92381:AB007956

R-HEM BB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969

10 R-HEM BB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840

R-HEM BB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:
15 97//Hs.16184:AJ001642

R-HEM BB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:
20 X98173

R-HEM BB1000404//ESTs//0.088:298:59//Hs.61607:AA032026

R-HEM BB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591

25 R-HEM BB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:
89//Hs.154326:D42087

30 R-HEM BB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!!
[H.sapiens]//0.30:214:63//Hs.142209:AA873303

R-HEM BB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990

35 R-HEM BB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221

R-HEM BB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438

40 R-HEM BB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396

R-HEM BB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:
45 90//Hs.40100:AB002390

R-HEM BB1000487//EST//0.78:87:68//Hs.134601:AI081506

50 R-HEM BB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:
AF088219

R-HEM BB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:
55 76//Hs.113283:AF018080

R-HEM BB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125

EP 1 074 617 A2

- R-HEM BB1000510//EST//1.4e-45:139:97//Hs.152260:AA489703
- 5 R-HEM BB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087
- 10 R-HEM BB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080
- R-HEM BB1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099
- 15 R-HEM BB1000550//EST//2.9e-11:113:79//Hs.161503:N68662
- R-HEM BB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:AF052288
- 20 R-HEM BB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986
- R-HEM BB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258
- 25 R-HEM BB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709
- R-HEM BB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618
- 30 R-HEM BB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247
- R-HEM BB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895
- 35 R-HEM BB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704
- R-HEM BB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391
- 40 R-HEM BB1000598//Human anti secretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199
- 45 R-HEM BB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125
- R-HEM BB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249
- 50 R-HEM BB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152
- R-HEM BB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531
- 55 R-HEM BB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522

EP 1 074 617 A2

R-HEM BB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582

R-HEM BB1000643//ESTs//0.0049:191:62//Hs.55445:W31963

5 R-HEM BB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100

10 R-HEM BB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939

R-HEM BB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988

15 R-HEM BB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705

R-HEM BB1000673//EST//0.58:46:82//Hs.142286:AA338293

20 R-HEM BB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454

R-nnnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723

25 R-HEM BB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219

30 R-HEM BB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412

R-HEM BB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403

35 R-HEM BB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306

40 R-HEM BB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881

R-HEM BB100073 8//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121493:D25272

45 R-HEM BB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925

R-HEM BB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522

50 R-HEM BB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445

R-HEM BB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541

55 R-HEM BB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771

EP 1 074 617 A2

- R-HEM BB1000790//PLATELET GLYCOPROTEIN V PRECURSORY//1.3e-37:193:75//Hs.73734:Z23091
- 5 R-HEM BB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718
- R-HEM BB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961
- 10 R-HEM BB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219
- R-HEM BB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447
- 15 R-HEM BB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124
- R-HEM BB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219
- 20 R-HEM BB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881
- R-HEM BB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176
- 25 R-HEM BB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545
- R-HEM BB1000840//ATPase, Na⁺/K⁺ transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876
- 30 R-HEM BB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:AB011137
- 35 R-HEM BB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599
- R-HEM BB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942
- 40 R-HEM BB1000876//EST//0.0022:211:63//Hs.125552:AA884141
- 45 R-HEM BB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247
- R-HEM BB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740
- 50 R-HEM BB1000888//EST//8.2e-07:196:64//Hs.118276:W15258
- R-HEM BB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.1e-46:327:83//Hs.51048:X68830
- 55

EP 1 074 617 A2

R-HEM BB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881

R-HEM BB1000908//EST//0.95:27:100//Hs.142568:AA285066

5 R-HEM BB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983

R-HEM BB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:
10 73//Hs.149323:AB002325

R-HEM BB1000915//ESTs//0.00018:188:61//Hs.44847:AI222742

15 R-HEM BB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:
84//Hs.127649:AB007874

R-HEM BB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784

20 R-HEM BB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350:
91//Hs.49163:AA532881

25 R-HEM BB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:
86//Hs.23094:MI9503

R-HEM BB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354

30 R-HEM BB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007

R-HEM BB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242

35 R-HEM BB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369

R-HEM BB1000991//EST//0.99:58:72//Hs.100246:T23625

40 R-HEM BB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:
70//Hs.154103:AF061258

45 R-HEM BB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112

R-HEM BB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//2.3e-25:339:
71//Hs.129992:H58762

50 R-HEM BB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214

R-HEM BB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814

55 R-HEM BB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:
76//Hs.113283:AF018080

EP 1 074 617 A2

- R-HEMBB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562
- 5 R-HEMBB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385
- R-HEMBB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975
- 10 R-HEMBB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107
- R-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497:91//Hs.15832:AB014518
- 15 R-HEMBB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:AB007944
- 20 R-HEMBB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785
- R-HEMBB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381
- 25 R-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803
- R-HEMBB1001096//Human HsLIM15 mRNA for HsLiml5, complete cds//1.2e-20:233:70//Hs.37181:D64108
- 30 R-HEMBB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353
- 35 R-HEMBB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080
- 40 R-HEMBB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426
- R-HEMBB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092
- 45 R-HEMBB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942
- R-HEMBB1001126
- 50 R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077
- R-HEMBB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962
- 55 R-HEMBB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881

EP 1 074 617 A2

R-HEMBB1001151

5 R-HEMBB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197

R-HEMBB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878

10 R-nnnnnnnnnnnn//ESTs//3.5e-41:233:93//Hs.129218:AA991162

R-HEMBB1001177

15 R-HEMBB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349

R-HEMBB1001199

20 R-HEMBB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183

R-HEMBB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549

25 R-HEMBB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573

30 R-HEMBB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//3.1e-44:298:87//Hs.103458:X53795

R-HEMBB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817

35 R-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]//3.8e-80:400:96//Hs.71873:AA148213

40 R-HEMBB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560

R-HEMBB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236

45 R-HEMBB1001253//EST//0.0011:84:77//Hs.124579:AA853987

R-HEMBB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268

50 R-HEMBB1001267//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0501//1.3e-50:524:73//Hs.159897:AB007970

55 R-HEMBB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087

R-HEMBB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412

EP 1 074 617 A2

R-HEM BB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]/2.6e-104:515:97//Hs.16606:W81021

5 R-HEM BB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840

R-HEM BB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112

10 R-HEM BB1001302

R-HEM BB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

15 R-HEM BB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627

R-HEM BB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627

20 R-HEM BB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873

R-HEM BB1001326//ESTs//0.85:174:62//Hs.133487:AI393754

25

R-HEM BB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]/6.5e-61:313:96//Hs.43071:AA206222

30 R-HEM BB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365

R-HEM BB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639

35 R-HEM BB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470

R-HEM BB1001346

40 R-HEM BB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354

R-HEM BB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721

45 R-HEM BB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/3.0e-12:129:79//Hs.9792:AA027055

50 R-HEM BB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087

R-HEM BB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617

55 R-HEM BB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219

EP 1 074 617 A2

- R-HEM BB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205
- R-HEM BB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699
- 5 R-HEM BB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970
- R-HEM BB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350
- 10 R-HEM BB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:365:58//Hs.389:
X76342
- 15 R-HEM BB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644
- R-HEM BB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651
- 20 R-HEM BB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846
- R-HEM BB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317
- 25 R-HEM BB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201
- R-HEM BB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236
- 30 R-HEM BB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515
- R-HEM BB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293
- 35 R-HEM BB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:
AB007881
- 40 R-HEM BB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:61//Hs.13275:
AI341468
- R-HEM BB1001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:
83//Hs.26799:W74481
- 45 R-HEM BB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515
- 50 R-HEM BB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:
92//Hs.17630:AB018280
- 55 R-HEM BB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN
CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915
- R-HEM BB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159

EP 1 074 617 A2

R-HEM BB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:
X99459

5 R-HEM BB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:
83//Hs.153014:AB002353

10 R-HEM BB1001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.5158:
AB007869

R-HEM BB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274

15 R-HEM BB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962

R-HEM BB1001564//EST//1.3e-35:141:81//Hs.162197:AA53521

20 R-HEM BB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:
85//Hs.146395:AB002329

25 R-HEM BB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944

R-HEM BB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219

30 R-HEM BB1001588//EST//8.3e-27:363:69//Hs.141603:N66015

R-HEM BB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184

35 R-HEM BB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044

R-HEM BB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888

40 R-HEM BB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:
D25272

R-HEM BB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082

45 R-HEM BB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633

R-HEM BB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813

50 R-HEM BB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438

R-HEM BB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577

55 R-HEM BB1001668//ESTs//0.73:212:62//Hs.8928:N32572

R-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573:

EP 1 074 617 A2

97//Hs.24439:AB014546

5 R-HEMBB1001684//ESTs, Moderately similar to Tbcl [M.musculus]//5.4e-106:523:
97//Hs.26939:AA804534

10 R-HEMBB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358

R-HEMBB1001695//ESTs//3.7e-101:539:94//Hs.78289:R60867

15 R-HEMBB1001704//EST//0.96:248:57//Hs.163025:AA703038

R-HEMBB1001706//ESTs//1.3e-39:308:81//Hs.141318:N71080

20 R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:
277:73//Hs.142764:AA205569

R-HEMBB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645

25 R-HEMBB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
[Homo sapiens]//8.6e-11:158:71//Hs.141263:H64113

R-HEMBB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403

30 R-HEMBB1001747//EST//9.9e-55:293:81//Hs.112866:AA620488

R-HEMBB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25287

35 R-HEMBB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059

R-HEMBB1001756//EST//2.6e-06:165:64//Hs.121195:AA757211

40 R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:
74//Hs.70008:L00352

45 R-HEMBB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369

R-HEMBB1001785//ESTs//0.040:390:58//Hs.116651:AA993406

50 R-HEMBB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253

R-HEMBB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391

55 R-HEMBB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247

R-HEMBB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:

EP 1 074 617 A2

76//Hs.23094:M19503

5 R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209

10 R-HEM BB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288:73//Hs.67619:AB007957

R-HEM BB1001839

15 R-HEM BB1001850//EST//0.020:119:68//Hs.32767:H38125

R-HEM BB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI357539

20 R-HEM BB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106

R-HEM BB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397

25 R-HEM BB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434

R-HEM BB1001872//EST//0.85:156:64//Hs.119501:AA487980

30 R-HEM BB1001874//EST//0.64:107:70//Hs.147482:AI215572

R-HEM BB1001875//EST//0.079:199:59//Hs.121810:AA775240

35 R-HEM BB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081

R-HEM BB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310

40 R-HEM BB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191

R-HEM BB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725

45 R-HEM BB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915

R-HEM BB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216

50 R-HEM BB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750

55 R-HEM BB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897

R-HEM BB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390

EP 1 074 617 A2

- R-HEM BB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRrp129//7.4e-38:531:70//Hs.153086:Y11251
- 5 R-HEM BB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325
- 10 R-HEM BB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875
- R-HEM BB1001944//EST//0.034:228:57//Hs.93664:N23366
- 15 R-HEM BB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875
- R-HEM BB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589
- 20 R-HEM BB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998
- R-HEM BB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788
- 25 R-HEM BB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:83//Hs.74554:D38522
- R-HEM BB1001957//EST//4.8e-50:382:81//Hs.149580:AI281881
- 30 R-HEM BB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972
- R-HEM BB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296:88//Hs.153468:AB011147
- 35 R-HEM BB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531
- 40 R-HEM BB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475
- R-HEM BB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572
- 45 R-HEM BB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223
- R-HEM BB1001996
- 50 R-HEM BB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798
- R-HEM BB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-18:222:71//Hs.103948:K00627
- 55 R-HEM BB1002005//EST//2.2e-41:339:80//Hs.160833:AI345334

EP 1 074 617 A2

R-HEM BB1002009//EST//2.9e-44:245:94//Hs.28788:R66896

R-HEM BB1002015//EST//0.0027:198:63//Hs.160868:AI359052

5 R-HEM BB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900

R-HEM BB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426

10 R-HEM BB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638

R-HEM BB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301:85//Hs.113283:AF018080

15 R-HEM BB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638

R-HEM BB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840

20 R-HEM BB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671

R-HEM BB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.129735:AF010144

25 R-HEM BB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193

30 R-HEM BB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881

R-HEM BB1002115

35 R-HEM BB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814

R-HEM BB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//1.4e-45:281:88//Hs.125231:AF068006

40 R-HEM BB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553

R-HEM BB1002189//H.sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073

45 R-HEM BB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185

50 R-HEM BB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934

R-HEM BB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881

55 R-HEM BB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841

EP 1 074 617 A2

- R-HEM BB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584
- 5 R-HEM BB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631
- R-HEM BB1002249//ESTs//5.2e-16:325:64//Hs.156253:AI334807
- 10 R-HEM BB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590:88//Hs.23094:M19503
- R-HEM BB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363
- 15 R-HEM BB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112
- 20 R-HEM BB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223
- R-HEM BB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305
- 25 R-HEM BB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67//Hs.155174:AB007892
- R-HEM BB1002327//EST//0.042:249:61//Hs.121097:AA714637
- 30 R-HEM BB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312
- R-HEM BB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228
- 35 R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46:84//Hs.42644:AJ010841
- 40 R-HEM BB1002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322
- R-HEM BB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613
- 45 R-HEM BB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:65//Hs.74554:D38522
- R-HEM BB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085
- 50 R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs.142296:AF072467
- 55 R-HEM BB1002383//ESTs//3.5e-108:520:98//Hs.45140:D80055
- R-HEM BB1002387

EP 1 074 617 A2

- 5 R-HEM BB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//2.3e-23:168:77//Hs.133526:N21103
- R-HEM BB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:
90//Hs.144563:AF057280
- 10 R-HEM BB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293
- R-HEM BB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:
87//Hs.153014:AB002353
- 15 R-HEM BB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:
71//Hs.154326:D42087
- 20 R-HEM BB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089
- R-HEM BB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083
- 25 R-HEM BB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176
- R-HEM BB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969
- 30 R-HEM BB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017
- R-HEM BB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:
T41142
- 35 R-HEM BB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615
- R-HEM BB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:
95//Hs.48827:AA873278
- 40 R-HEM BB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538
- 45 R-HEM BB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete
cds//0.50:142:69//Hs.159301:U43672
- 50 R-HEM BB1002531//EST//0.024:147:61//Hs.148305:AA909605
- R-HEM BB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478
- 55 R-HEM BB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259
- R-HEM BB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-
22:210:81//Hs.11896:T68813

EP 1 074 617 A2

R-HEM BB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.9e-45:344:
 82//Hs.51048:X68830
 5
 R-HEM BB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189
 R-HEM BB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045
 10
 R-HEM BB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138
 R-HEM BB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:
 15 87//Hs.154326:D42087
 R-HEM BB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424
 20 R-HEM BB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923
 R-HEM BB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881
 25 R-HEM BB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896
 R-HEM BB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
 [H.sapiens]//6.2e-07:140:70//Hs.155456:AA707265
 30 R-HEM BB1002613//Homo sapiens mRNA, chromosome 1 specific transcript
 KIAA0508//8.5e-47:278:83//Hs.159187:AB007977
 35 R-HEM BB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150
 R-HEM BB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-
 19:151:80//Hs.137574:AF055917
 40 R-HEM BB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247
 R-HEM BB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:
 45 AF088219
 R-HEM BB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881
 50 R-HEM BB1002677//ESTs//0.65:159:62//Hs.163517:AI419775
 R-HEM BB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//8.6e-54:543:
 75//Hs.2638:Z28339
 55 R-HEM BB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646

EP 1 074 617 A2

R-HEMBB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753

R-HEMBB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099

5 R-HEMBB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487

R-HEMBB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398

10 R-HEMBB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842

R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547

15 R-HEMBB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682

R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701

20 R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219

25 R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384:80//Hs.155533:X60152

R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901

30 R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:AB018304

35 R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165

R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350

40 R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531

R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065

45 R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099

50 R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241

55 R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713

R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:

EP 1 074 617 A2

86//Hs.70008:L00352

5 R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172

R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577

10 R-MAMMA1000133

R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017

15 R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0501//6.3e-40:288:78//Hs.159897:AB007970

R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881

20 R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA,
complete cds//1.5e-59:562:75//Hs.77579:AF013263

25 R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787

R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:
173:83//Hs.53531:AJ224162

30 R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus
gallus]//2.4e-07:63:90//Hs.90367:AI357069

35 R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611

R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054

40 R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881

R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.musculus]//1.4e-41:
272:90//Hs.68398:AA421103

45 R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425

R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946

50 R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:
86//Hs.15519:AB018315

55 R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA,
complete cds//2.2e-43:315:83//Hs.129708:AF064090

EP 1 074 617 A2

R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041

R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238

5 R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814

R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript
10 KIAA0508//2.7e-57:304:78//Hs.159187:AB007977

R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369

15 R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694

R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0487//3.1e-58:295:83//Hs.92381:AB007956

20 R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066

R-MAMMA1000287

25 R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892

R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067

30 R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251

35 R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434

R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491

40 R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:AA662998

R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881

45 R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525

50 R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159

R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs.11463:AA535912

55 R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:

EP 1 074 617 A2

82//Hs.154326:D42087

- 5 R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659
- R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523
- 10 R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065
- R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:92//Hs.32170:AB015132
- 15 R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AB01060
- R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POLYPROTEIN [Mus musculus]//9.1e-47:316:81//Hs.138698:N38973
- 20 R-MAMMA1000410//Archain//1.8e-40:443:74//Hs.33642:X81198
- R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:AB007958
- 25 R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099
- R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:282:82//Hs.97203:U83171
- 30 R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081
- 35 R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067
- R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390
- 40 R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452
- 45 R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461
- R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171
- 50 R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179
- 55 R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447
- R-MAMMA1000458

EP 1 074 617 A2

- R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176
- 5 R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361
- R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959
- 10 R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886
- R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759
- 15 R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219
- R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390
- 20 R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390
- R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267
- R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236
- 25 R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131
- R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561
- 30 R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211
- R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872
- 40 R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548
- R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219
- 45 R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042
- 50 R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267
- 55 R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105

EP 1 074 617 A2

R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180

R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361

5 R-MAMMA1000623

R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002

10 R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203

R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, partial//3.2e-43:
15 400:76//Hs.53531:AJ224162

R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

20 R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3'REGION
[Klebsiella pneumoniae]//8.4e-98:464:98//Hs.31431:AI022065

R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476

25 R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212

R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:
30 75//Hs.98938:AB002343

R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644

35 R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:
74//Hs.153563:AF011333

R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:
40 158:79//Hs.142764:AA205569

R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515

45 R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329

R-MAMMA1000723//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete
50 cds//5.6e-52:350:82//Hs.46328:D87942

R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267

R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893

55 R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN
CHROMOSOME III [Caenorhabditis elegans]//1.2e-35:371:74//Hs.141429:AA631915

EP 1 074 617 A2

R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253:98//Hs.31575:AF100141
 5
 R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//2.3e-116:557:98//Hs.71472:AA632288
 10
 R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205
 R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568:86//Hs.23094:M19503
 15
 R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627
 R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131
 20
 R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256
 R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:76//Hs.153014:AB002353
 25
 R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204
 R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439
 30
 R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150
 R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163
 35
 R-MAMMA1000802//Clathrin, light polypeptide (Lcb)//1.5e-45:358:76//Hs.73919:X81637
 R-MAMMA1000831//ESTs//1.3e-1,04:510:97//Hs.17494:AA572675
 40
 R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881
 R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902
 45
 R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//9.4e-44:363:79//Hs.96337:AA225358
 50
 R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097
 R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955
 55
 R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251

EP 1 074 617 A2

R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:91//Hs.40100:AB002390

5 R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212

R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI419311

10 R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922

R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//Hs.46918:AF052099

15

R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399

R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI032875

20

R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243

R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128

25

R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872:AB011166

30

R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107

R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI310215

35

R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329

R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093

40

R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634

R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989

45

R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs.108966:U48696

50

R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335

R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727

55

R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281

R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428

EP 1 074 617 A2

- 5 R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducible),
polypeptide 2//9.3e-79:567:80//Hs.1361:M55053
- 10 R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178
- 15 R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2
leukocyte antigen, antigen detected by monoclonal and antibody IA4))//7.5e-49:340:
85//Hs.103458:X53795
- 20 R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48:216:
85//Hs.153468:AB011147
- 25 R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881
- 30 R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204
- 35 R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39:338:
79//Hs.93121:AB018304
- 40 R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881
- 45 R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA,
complete cds//3.9e-50:445:77//Hs.77579:AF013263
- 50 R-MAMMA1001003//Sialophorin (gpL115, leukosialin, CD43)//4.1e-51:282:82//Hs.80738:
X52075
- 55 R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:97//Hs.25863:
AA630313
- 60 R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:
86//Hs.153563:AF011333
- 65 R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814
- 70 R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536
- 75 R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461
- 80 R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:91//Hs.40100:
AB002390
- 85 R-nnnnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650
- 90 R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881

EP 1 074 617 A2

- 5 R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]/1.7e-13:273:65//Hs.98738:AI015487
- R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532
- 10 R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748
- R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353
- 15 R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944
- R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503
- 20 R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222
- R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926
- 25 R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF035587
- 30 R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.61840:U28686
- R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576
- 35 R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.116007:S79267
- 40 R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750
- R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029
- 45 R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399
- R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179
- 50 R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131
- R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750
- 55 R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]/2.1e-91:430:99//Hs.129982:

EP 1 074 617 A2

AI420970

- 5 R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251
- R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959
- 10 R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519
- R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.musculus]//2.6e-80:358:96//Hs.163827:AA074202
- 15 R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348
- R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637
- 20 R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148
- R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293
- 25 R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202
- R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315
- 30 R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701
- R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619
- 35 R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307
- R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569
- 40 R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149
- R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561
- 45 R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001
- 50 R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30643
- R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144
- 55 R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371

EP 1 074 617 A2

- R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876
- 5 R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:AB011135
- R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426
- 10 R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.46468:U45984
- 15 R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.55771:AF004709
- R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471
- 20 R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426
- R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519
- 25 R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127
- R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478
- 30 R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322
- 35 R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216
- R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881
- 40 R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831
- R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275
- 45 R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957
- R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267
- 50 R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168
- R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618
- 55 R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67//Hs.155174:AB007892

EP 1 074 617 A2

- R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542
- 5 R-MAMMA1001465
- R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317
- 10 R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78//Hs.43681:AL022394
- 15 R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065
- R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522
- 20 R-MAMMA1001510
- R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242
- 25 R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969
- R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696
- 30 R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140
- 35 R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549:96//Hs.21635:AI417305
- R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441
- 40 R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792
- R-MAMMA1001604
- 45 R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]//1.9e-97:488:96//Hs.143263:AI057616
- 50 R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272
- 55 R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519:AB018315
- R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//6.8e-15:168:

EP 1 074 617 A2

73//Hs.115216:AA291074

- 5 R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377
- R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606
- 10 R-MAMMA1001649
- R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272:81//Hs.129735:AF010144
- 15 R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs.155464:AF088219
- R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248
- 20 R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.066:196:62//Hs.159161:X69550
- 25 R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081
- R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957
- 30 R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:89//Hs.3094:D31884
- 35 R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088
- R-MAMMA1001715//ESTs//1.2e-73:399:9311Hs.124620:AI082338
- 40 R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596
- R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]//3.7e-110:552:96//Hs.6923:AI161158
- 45 R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651
- R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666
- 50 R-MAMMA1001744
- R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817
- 55 R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041

EP 1 074 617 A2

R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413

5 R-MAMMA1001757//ESTs//1.0e-9.8:488:96//Hs.45184:C14904

R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI142276

10 R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847

R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299:85//Hs.149323:AB002325

15 R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825

R-MAMMA1001771//ESTS, Moderately similar to semaphorin B [M.musculus]//7.6e-43:257:91//Hs.7634:AA481246

20 R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272:86//Hs.73614:U83460

25 R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238

R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644

30 R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744

R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313

35 R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892

R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659

40 R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:87//Hs.44106:D86979

R-MAMMA1001818

45 R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881

R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs.32567:AF073519

50 R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140

55 R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83//Hs.43681:AL022394

EP 1 074 617 A2

R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811

R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461

5 R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:83//Hs.155464:AF088219

10 R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI148840

R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-31:262:77//Hs.5737:AB007944

15 R-nnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450:58//Hs.132206:AF039694

20 R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.9e-46:332:83//Hs.73614:U83460

R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.2e-46:429:78//Hs.2379:U23942

25 R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606

30 R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788

R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//6.7e-47:283:89//Hs.103458:X53795

35 R-nnnnnnnnnnnn//ESTs//0.043:134:65//Hs.145333:AI251374

40 R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801

R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.4e-18:174:77//Hs.139648:AB014606

45 R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790

50 R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]//6.7e-24:331:71//Hs.140506:AA308018

R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734

55 R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084

EP 1 074 617 A2

R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs.155464:AF088219

5 R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054

R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mRNA//3.7e-45:370:80//Hs.154069:U06452

10

R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223

R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412

15

R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs.32567:AF073519

20 R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.9e-37:316:74//Hs.10458:AF088219

R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881

25

R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979

R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:7811Hs/138596:N38806

30

R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875

35 R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887:AB013924

R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390

40

R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907

45

R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347

R-MAMMA1002118

50

R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081

R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//Hs.129735:AF010144

55

R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:AF035835

EP 1 074 617 A2

R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276

5 R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886

R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548

10 R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503

15 R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531:AJ224162

R-MAMMA1002158//ESTs//3-0e-40:313:83//Hs.118273:AA626040

20 R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509

25 R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs.92381:AB007956

30 R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734

R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038

35 R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026:AB014540

40 R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696

R-MAMMA1002236

45 R-MAMMA1002243

R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080

50 R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript

55 KIAA0487//1.6e-54:207:81//Hs.92381:AB007956

R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283

EP 1 074 617 A2

- R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772
- 5 R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141
- R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751
- 10 R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257:AI275982
- R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881
- 15 R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454
- R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153
- 20 R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359
- 25 R-MAMMA1002308
- R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs.154069:U06452
- 30 R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:M19503
- 35 R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094
- R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457:76//Hs.144563:AF057280
- 40 R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183
- R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084
- 45 R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658
- R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317
- 50 R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897
- 55 R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618
- R-MAMMA1002347//ESTS//1.5e-44:326:83//Hs.111723:H57439

EP 1 074 617 A2

- R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127
- 5 R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228
- R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390
- 10 R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367
- 15 R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217:88//Hs.73919:X81637
- R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080
- 20 R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475
- R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587
- 25 R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236
- 30 R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542
- R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs.155464:AF088219
- 35 R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061
- R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:83//Hs.86188:D87845
- 40 R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294
- 45 R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.115325:D84488
- R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588
- 50 R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477
- R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475
- 55 R-MAMMA1002434//ESTS, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-106:521:98//Hs.112152:AA487348

EP 1 074 617 A2

- 5 R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!!
[H.sapiens]//4.7e-37:374:68//Hs.157142:U85996
- 10 R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript
KIAA0485//2.0e-60:323:81//Hs.89121:AB007954
- 15 R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076
- R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-
NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94570:
AI192106
- 20 R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//3.4e-31:263:79//Hs.38687:AA744496
- 25 R-MAMMA10024807//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//1.0e-34:159:79//Hs.133526:N21103
- R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:
560:97//Hs.155223:AF055460
- 30 R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293
- R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:
58//Hs.37035:U07664
- 35 R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277
- 40 R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma)
mRNA, complete cds//3.9e-103:529:95//Hs.18858:AF065214
- R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:
88//Hs.153468:AB011147
- 45 R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851
- 50 R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//1.0e-12:280:65//Hs.12725:T65058
- R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681
- 55 R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693
- R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433

EP 1 074 617 A2

- R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371
- R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258
- 5 R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide
6//2.9e-21:177:75//Hs.1360:M29874
- 10 R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737
- R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369
- 15 R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible),
polypeptide 2//4.2e-46:424:75//Hs.1361:M55053
- R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389
- 20 R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:
73//Hs.108287:L27670
- 25 R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306
- R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081
- 30 R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881
- R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.3e-
35:308:79//Hs.93332:AA811920
- 35 R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-
57:283:86//Hs.115325:D84488
- 40 R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:
AB002390
- R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421
- 45 R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915
- R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776
- 50 R-MAMMA1002655
- R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:
55 75//Hs.97476:AB007886
- R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:

EP 1 074 617 A2

82//Hs.154326:D42087

5 R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5
[C.elegans]//5.3e-108:544:96//Hs.16464:W19606

R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213

10 R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544:
96//Hs.3363:D86987

R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385

15

R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675

R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510

20

R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//6.9e-70:353:96//Hs.138404:R70986

25

R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234

R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858

30

R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:
89//Hs.153563:AF011333

R-MAMMA1002727//ESTs//2.9e-84:395:10011Hs.162826:AA679571

35

R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs.155464:
AF088219

40

R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757

R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907

45

R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-
40:330:80//Hs.154069:U06452

50

R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//4.5e-40:369:77//Hs.105292:AA504776

R-MAMMA1002758

55

R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281

R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651

EP 1 074 617 A2

R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272

5 R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750

R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145

10 R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812

R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198

15 R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260

R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:AI248319

20 R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:AI281881

R-MAMMA1002835

25 R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723

R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395

30 R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238

R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081

35 R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067

R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941

40 R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:AI243592

R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194

45 R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:AI365871

R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs.155464:AF088219

50 R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811

R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//4.2e-92:438:99//Hs.155871:AA533783

55 R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322:

EP 1 074 617 A2

80//Hs.26929:AF008915

R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087

5

R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179

R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:
D80002

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R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:AI281881

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R-MAMMA1002938

R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556:
85//Hs.23094:M19503

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R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243

R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:
77//Hs.153014:AB002353

25

R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081

30

R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:
95//Hs.94396:AA399630

R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835

35

R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279

R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA,
complete cds//2.1e-41:402:67//Hs.133089:AF064019

40

R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179

45

R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:AI127857

R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617

50

R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus
norvegicus]//1.4e-53:320:90//Hs.92023:AI022248

R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189

55

R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268

EP 1 074 617 A2

R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315

5 R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//3.5e-27:257:77//Hs.96337:AA225358

R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321

10 R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160

R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940

15 R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:AI002941

R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862

20 R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348

R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:AI281881

25 R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:AI038559

R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:
30 545:93//Hs.13755:AA878911

R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969

35 R-MAMMA1003089//ESTS, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
[H.sapiens]//1.4e-34:421:70//Hs.161959:AA493652

R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651

40 R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283

R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366

45 R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788

R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125

50 R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI149537

R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:
55 61//Hs.152213:L20861

R-nnnnnnnnnnnnn

EP 1 074 617 A2

R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]/2.0e-87:524:89//Hs.6884:W30736

5 R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587:94//Hs.108112:AF070640

10 R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312

R-NT2RM4000027

15 R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663

R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:AI86169

20 R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379

R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds/4.0e-113:549:97//Hs.95665:AF070639

25 R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817

R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708

30 R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI052312

R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]/1.9e-99:536:92//Hs.127810:AI246301

35

R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397

40 R-nnnnnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962

R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:AI382160

45 R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]/4.1e-99:542:93//Hs.6366:AA614113

R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723

50 R-NT2RM400019911ESTs//10.020:95:6511Hs.146203:AI254528

R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876

55 R-NT2RM4000202//Small inducible cytokine A5 (RANTES)/4.3e-37:330:77//Hs.155464:AF088219

EP 1 074 617 A2

R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546:94//Hs.111138:AB018255

5 R-NT2RM4000215

R-nnnnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA477760

10 R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)//0.00020:174:66//Hs.235:X51602

R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031

15

R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs.119498:AF000974

20 R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:AI378742

R-NT2RM4000290//ESTs//4.0e-87:435:96//Hs.162592:AA594128

25 R-NT2RM4000324//ESTs//2.2e-80:413:96//Hs.12313:R43673

R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286:87//Hs.155464:AF088219

30

R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60:452:84//Hs.73919:X81637

R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H.sapiens]//2.5e-117:579:96//Hs.5216:AA534881

35

R-NT2RM4000354//ESTs//2.1e-85:406:99//Hs.126774:AI224479

40 R-NT2RM4000356//ESTs//7.9e-109:548:96//Hs.44278:AA418063

R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577:95//Hs.8152:AB014542

45

R-NT2RM4000368//ESTs//2.2e-61:310:97//Hs.143611:M78140

R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521:92//Hs.41793:AA775879

50

R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99:524:94//Hs.5249:U55977

55

R-NT2RM4000414//EST//2.7e-06:196:64//Hs.136648:AA688285

EP 1 074 617 A2

R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.elegans]//5.4e-75:470:90//Hs.69235:AA192359

5 R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112:69//Hs.19949: X98173

R-NT2RM4000433//ESTs//2.7e-100:479:98//Hs.24553:AI150687

10

R-NT2RM4000457//ESTs//5.1e-107:535:95//Hs.7579:AA775865

15 R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//6.0e-99:492:96//Hs.21090:AA418587

R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens]//2.2e-102:493:97//Hs.111279:W84558

20

R-NT2RM4000496

R-NT2RM4000511//EST//5.1e-43:326:81//Hs.157658:AI358465

25

R-NT2RM4000514//ESTS//1.7e-112:552:96//Hs.6686:AA205496

30 R-ntntntntntntntntntntnt//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae]//1.4e-60:343:93//Hs.16014: AA074879

35 R-NT2RM4000520//ESTs//2.7e-55:266:100//Hs.99838:AA204731

R-NT2RM4000531//ESTs//2.0e-88:502:91//Hs.13110:T67461

40 R-NT2RM4000532//ESTs//0.47:290:58//Hs.148753:T91777

R-NT2RM4000534//EST//0.00025:303:60//Hs.162809:AA632198

45 R-NT2RM4000585//EST//0.28:63:77//Hs.150024:AI291981

R-NT2RM4000590//ESTs//5.8e-65:320:98//Hs.116017:AA613437

50 R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189:64//Hs.16349: AB007891

R-NT2RM4000603//ESTs//4.6e-68:356:96//Hs.48855:AA134589

55 R-ntntntntntntntntntntnt//ESTs//1.5e-89:431:97//Hs.26117:W16697

R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHETASE

EP 1 074 617 A2

[Escherichia coli]/1.4e-102:519:96//Hs.14779:N64822

R-NT2RM4000674//ESTs//5.1e-78:398:97//Hs.8268:N70144

5

R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C.elegans]/2.9e-115:550:98//Hs.11820:AA205531

10

R-NT2RM4000698//ESTs//2.0e-17:130:87//Hs.86420:AA927510

R-nnnnnnnnnnnnn

15

R-NT2RM4000712//EST//0.99:103:65//Hs.114039:AA701128

R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]/2.2e-103:519:95//Hs.6823:W18181

20

R-NT2RM4000733//ESTs//8.7e-88:429:98//Hs.72185:AA465311

25

R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6e-105:536:95//Hs.137168:AB018303

R-NT2RM40007.41//ESTs//0.99:266:58//Hs.142718:AA034046

30

R-NT2RM4000751//ESTs//1.6e-20:351:66//Hs.43145:AA776988

R-NT2RM4000764

35

R-NT2RM4000778//EST//0.066:254:61//Hs.148232:AA904174

R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.3e-106:546:94//Hs.18586:AB007920

40

R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.5e-40:424:73//Hs.154069:U06452

45

R-NT2RM4000790//EST//9.0e-48:259:94//Hs.159694:AI417008

R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//Hs.20991:D31891

50

R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520

55

R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249:M21868

R-NT2RM4000813

EP 1 074 617 A2

R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:AI219667

5 R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031

10 R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864

R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597

15 R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343

R-nnnnnnnnnnnnn

20 R-NT2RM4000895//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.3e-96:450:99//Hs.142076:AA604514

R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262

25 R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887

R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647

30 R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:AA650126

35 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:AB018272

R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:AB014539

40 R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352

45 R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.32170:AB015132

R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300

50 R-nnnnnnnnnnn//ESTs//3.4e-91:439:99//Hs.103177:W72798

R-NT2RM4001092//ESTs//1.4e-86:517:8911Hs.132969:Z78324

55 R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962

EP 1 074 617 A2

R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276

5 R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311

R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848

10 R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085

R-NT2RM4001187//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!!
[H.sapiens]//9.2e-43:273:91//Hs.109005:N31174

15 R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:
70//Hs.2379:U23942

20 R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849

R-NT2RM4001203

R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307

25 R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410

R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677

30 R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184

R-NT2RM4001309

35 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857

R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899

40 R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352

R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces
45 cerevisiae]//1.9e-105:522:97//Hs.18442:AI129307,

R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339

50 R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476

R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211

55 R-NT2RM4001382

R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507

EP 1 074 617 A2

R-NT2RM4001410//EST//0.13:50:82//Hs.157675:AI358790

5 R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk
[M.musculus]//4.0e-102:539:94//Hs.15744:AI055859

R-NT2RM4001412

10

R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA775895

R-NT2RM4001437//EST//0.017:169:67//Hs.13207:F10054

15

R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE,
MITOCHONDRIAL [S.cerevisiae]//7.4e-108:544:94//Hs.7558:AA526812

20

R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277

R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA969739

25

R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:
D26067

30

R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547:
93//Hs.153121:AB014585

R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664

35

R-NT2RM40015227//Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.155464:
AF088219

40

R-NT2RM40015577//ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21:165:
83//Hs.29134:H43072

R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027

45

R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4.
Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced
Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,
6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker
50 DXS8032//2.7e-43:446:72//Hs.4943:Z98046

R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.86959:AA888009

55

R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946

R-nnnnnnnnnnnnn

EP 1 074 617 A2

R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171

5 R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:AI358871

R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565:95//Hs.23255:AB018334

10 R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079

R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957

15 R-NT2RM4001650

R-NT2RM4001662

20 R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230:70//Hs.7764:AB007938

25 R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:AI367496

R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440

30 R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686

R-nnnnnnnnnnn//ESTs//6.5e-104:487:99//Hs.153581:AA630465

35 R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-108:563:94//Hs.18510:AA522887

R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083:124:68//Hs.120980:S83390

40 R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200

45 R-NT2RM4001754//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629

R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:AI290740

50 R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270

55 R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956

R-NT2RM4001810//ESTs//1.3e-65:346:95//Hs.131915:W22567

EP 1 074 617 A2

- R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:AI089920
- 5 R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839
- R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551
- 10 R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070
- R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619
- 15 R-NT2RM4001842//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
[H.sapiens]//4.1e-10:274:62//Hs.161959:AA493652
- R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif
20 [C.elegans]//3.0e-43:292:86//Hs.14202:N46000
- R-nnnnnnnnnnnn//ESTs//6.2e-104:495:98//Hs.118686:AA682280
- 25 R-NT2RM40018657/Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:
592:97//Hs.61628:Y17711
- R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252
- 30 R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149
- R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178
- 35 R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//1.2e-105:535:95//Hs.30991:AA994438
- 40 R-NT2RM4001930//ESTs//4.1-84:425:96//Hs.80042:N63143
- R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893
- 45 R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:
95//Hs.118631:AF098162
- R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268
- 50 R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:
95//Hs.3385:N25917
- 55 R-nnnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:
98//Hs.8772:AA521097

EP 1 074 617 A2

R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265

5 R-NT2RM4001984

R-NT2RM4001987

10 R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528

R-NT2RM4002018

15 R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087

R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435

20 R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226

R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887

25 R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179

R-nnnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:AF071309

30 R-NT2RM4002067//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629

35 R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96//Hs.109274:AA193416

R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655

40 R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528

R-nnnnnnnnnnnn//ESTs//1.0:95:69//Hs.25897:W65409

45 R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620

R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712

50 R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987

R-NT2RM4002146//ESTs//1.9e-93:43 9:99//Hs.119295:AA442090

55 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535

EP 1 074 617 A2

R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:
 72//Hs.154103:AF061258
 5
 R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400
 R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343
 10
 R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678
 R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079
 15
 R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND
 [Drosophila melanogaster]//5.1e-112:569:95//Hs.23900:U82984
 20
 R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-
 1, 2-N-acetylglucosaminyltransferase [C.elegans]//1.1e-100:544:93//Hs.27567:W72190
 R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:
 25 AF088219
 R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864
 30
 R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263
 R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638
 35
 R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461
 R-NT2RM4002294
 40
 R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164
 R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498
 45
 R-nnnnnnnnnnnn//ESTs//5.0e-59:283:100//Hs.125048:AA682913
 R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:
 50 66//Hs.155129:M77198
 R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:
 97//Hs.26163:AB014549
 55
 R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594
 R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884

EP 1 074 617 A2

- R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328
- 5 R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5
[C.elegans]//1.3e-97:473:98//Hs.16464:W19606
- R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677
- 10 R-NT2RM4002446
- R-NT2RM4002452//EST//1.0:164:60//Hs.116619:AA668142
- 15 R-NT2RM4002457
- R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890
- 20 R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-
103:507:97//Hs.8765:AF083255
- 25 R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:
98//Hs.94781:AB014591
- R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884
- 30 R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029
- R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA464464
- 35 R-nnnnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor
[H.sapiens]//1.4e-73:360:91//Hs.31030:H50467
- 40 R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788
- R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057
- 45 R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312
- R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-
ACETYL GALACTOSAMINYLTRANSFERASE [Bos taurus]//2.3e-89:435:97//Hs.15830:
50 AA165698
- R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569
- 55 R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus
aquaticus thermophilus]//9.6e-28:194:87//Hs.59346:AI126802

EP 1 074 617 A2

R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096

R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081

5

R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366:67//Hs.54488:X69115

R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713

10

R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290

15

R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//4.3e-64:309:98//Hs.6216:AF061749

R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798

20

R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910

25

R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//2.3e-35:199:94//Hs.41793:AA775879

R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus]//1.4e-78:383:98//Hs.58254:W72881

30

R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097

35

R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.54877:AF050078

R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.102576:AJ010230

40

R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338

45

R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064

R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757

50

R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827

R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419

55

R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356

EP 1 074 617 A2

- 5 R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]/1.9e-19:153:86//Hs.5268:W22670
- R-nnnnnnnnnnn//ESTs//1.0e-55:293:95//Hs.14570:AI422099
- 10 R-nnnnnnnnnnnnn//ESTs//0.24:354:59//Hs.157564:AI356513
- R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]/3.0e-89:457:95//Hs.3832:AI208601
- 15 R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548
- R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA040820
- 20 R-NT2RP2000161//EST5//1.6e-99:492:97//Hs.21738:AI188190
- R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI143741
- 25 R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373
- R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510
- 30 R-NT2RP2000205//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/1.4e-80:415:95//Hs.11807:T86897
- R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)//1.1e-57:306:94//Hs.79402:AC004382
- 35 R-NT2RP2000232
- 40 R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:AI090683
- R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379
- 45 R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]/1.3e-95:454:99//Hs.102057:AA649005
- R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:AI126840
- 50 R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649
- R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]/8.4e-59:298:96//Hs.16085:AI261382
- 55 R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635

EP 1 074 617 A2

R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865

5 R-NT2RP2000289

R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951:AA574249

10

R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712

15 R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:93//Hs.58218:U82381

20 R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs//2.9e-71:342:98//Hs.87684:AL022398

25 R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441

30 R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:94//Hs.76556:U83981

35 R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103

R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010

40

R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324

45 R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:90//Hs.5819:AF102265

R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65:362:93//Hs.22197:AI151425

50

R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:92//Hs.21938:W81045

55

R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013

EP 1 074 617 A2

R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078

R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI290215

5 R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896

10 R-nnnnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348

R-NT2RP2000523

15 R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144

R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446

20 R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514

25 R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222

R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275

30 R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396

R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767

35 R-NT2RP2000678//ESTs//2.6e-53:271:9611Hs.23790:N99347

R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368

40 R-NT2RP2000715//EST//1.2e-87:418:9911Hs.139425:AA429279

R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965

45 R-NT2RP2000758//ESTS//1.0:187:61//Hs.10545:N62642

R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419

50 R-NT2RP2000809

R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745

55 R-nnnnnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404

R-NT2RP2000816//ESTS//0.45:100:69//Hs.147529:AA458918

EP 1 074 617 A2

R-NT2RP2000819

5 R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511

R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6

10 PRECURSOR//4.6e-10:247:66//Hs.29352:M31165

R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:AI206552

15 R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345

R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615:AB018284

20 R-NT2RP2000892//ESTs//2.8e-50:25 8:96//Hs.119238:AA476267

R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266

25 R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477

30 R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822:AB018298

R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021

35 R-NT2RP2000970//EST//8-7e-06:255:62//Hs.149202:AI246481

R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537

40 R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521

45 R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643

R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660

50 R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108

R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665

55 R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068

R-NT2RP2001119

EP 1 074 617 A2

5 R-NT2RP2001127//Homo sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348
 R-NT2RP2001137
 10 R-NT2RP2001149//ESTs//5.1e-66:324:9711Hs.27475:AA704512
 R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:AI188145
 15 R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247:AB007949
 R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287
 20 R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510
 R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402
 25 R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358
 R-NT2RP2001233//ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80//Hs.44014:AA632298
 30 R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996
 R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353
 35 R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229
 40 R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775
 R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665
 45 R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205
 R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]//2.3e-43:238:93//Hs.106632:N25679
 50 R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138
 R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178
 55 R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028

EP 1 074 617 A2

R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038

5 R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG
PRECURSOR [H.sapiens]//3.9e-74:411:93//Hs.47305:AA195153

R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875

10 R-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus
auratus]//5.2e-97:469:97//Hs.20483:AA522505

R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N32030

15

R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431

R-NT2RP2001427//EST//1.7e-1 1:107:84//Hs.148584:AI201728

20

R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114:558:97//Hs.7627:
AI341556

25

R-NT2RP2001440//EST//0.17:192:58//Hs.133442:AI061394

/

R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453

30

R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:AI076765

R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:AI079539

35

R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255:83//Hs.155464:
AF088219

R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513

40

R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146

R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-
106:545:95//Hs.4277:Y14494

45

R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240

50

R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3)
mRNA, complete cds//1.9e-15:99:95//Hs.99742:AF035586

R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816

55

R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-
76:387:96//Hs.67619:AB007957

EP 1 074 617 A2

R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193:60//Hs.119:
D14661

5 R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T58884

R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:AI369995

10 R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:AI393767

R-NT2RP2001613

15 R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294

R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090

20 R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:AI370845

R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:AI201336

25 R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:AI125323

R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579

30 R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538

R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI147100

35 R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840

R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:
40 519:96//Hs.47504:AF091754

R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037

45 R-NT2RP2001861

R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:AI002941

50 R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088

R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110:
55 556:95//Hs.23159:AA113849

R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724

EP 1 074 617 A2

R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423

R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI097268

5 R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087

R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:AI032180

10 R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594

R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588

15 R-NT2RP2001969

R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745

20 R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1
[M.musculus]//8.3e-15:118:89//Hs.18760:AA166678

25 R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:AI378233

R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332

30 R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627

R-NT2RP2002041

35 R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:AA825938

R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA629895

40 R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068

R-NT2RP2002066//ESTs//1.9e-87:459:93//Hs.118871:AA846091

45 R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T92265

R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:178:
87//Hs.11039:AF052183

50 R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI350524

R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e-60:376:
89//Hs.155218:AJ007509

55 R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:AI123000

EP 1 074 617 A2

R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA525134

5 R-NT2RP2002137//Deoxycytidine kinase//0.29:183:62//Hs.709:M60527

R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA523268

10 R-NT2RP2002172//EST//0.69:53:75//Hs.156238:AI334495

R-NT2RP2002185//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.4e-54:269:98//Hs.107201:W52859

15 R-NT2RP2002192//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-15:245:71//Hs.87578:AI125363

20 R-NT2RP2002193//ESTs//3.5e-79:45 3:90//Hs.76578:AI290672

R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:AI003946

25 R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287499

R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA642341

30 R-nnnnnnnnnnnn//ESTs, Highly similar to co-repressor protein [M.musculus]//5.4e-48:238:99//Hs.22583:AA188168

R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15:131:83//Hs.150595:AF005418

35 R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:548:91//Hs.92137:M19720

40 R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-100:550:91//Hs.4029:Z78373

45 R-NT2RP2002292//ESTs, Weakly similar to F13B12.1 [C.elegans]//3.2e-92:482:93//Hs.5570:AI377863

R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//4.1e-103:527:94//Hs.24812:AF069532

50 R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:AI368015

55 R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.2e-112:567:95//Hs.31034:AB015594

EP 1 074 617 A2

R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA767372

5 R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA,
complete cds//1.2e-103:600:89//Hs.109051:AF038958

R-NT2RP2002394//ESTs//0.11:158:65//Hs.28792:AI343467

10 R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W22815

R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33:285:
80//Hs.15731:AB011135

15

R-NT2RP2002439//ESTs//3.2e-12:134:76//Hs.32246:AA464020

R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97521

20

R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:AI362230

R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W27233

25

R-nnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//9.9e-
115:605:92//Hs.125856:AB005289

30

R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:N73180

R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60838

35

R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107:583:
91//Hs.23255:AB018334

R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA205305

40

R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:AA533090

R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//2.6e-109:570:
93//Hs.49476:AF009314

45

R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:86//Hs.80961:U60325

50

R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.5e-
118:564:97//Hs.94549:AA149547

R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA994783

55

R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:N40170

EP 1 074 617 A2

R-NT2RP2002609//ESTs//1.9e-104:568:92//Hs.9175:AI184220

R-NT2RP2002618//ESTs//0.014:493:57//Hs.96322:AA541615

5 R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI281881

R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA179944

10 R-NT2RP2002672

R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB//0.99:184:63//Hs.50727:U43572

15 R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA483223

R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210

20 R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626

R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300

25 R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108

30 R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352

R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131

35 R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042

R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124

40 R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:H03587

R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94//Hs.17481:AF070537

45 R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124

50 R-NT2RP2002839//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-100:501:97//Hs.136202:AA206578

R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031

55 R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870

EP 1 074 617 A2

R-NT2RP2002880

R-NT2RP2002891

5 R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894

R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143

10 R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096

R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771

15 R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480

R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060

20 R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213

R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578:97//Hs.106290:AI125291

25 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329

30 R-NT2RP2002993//ESTs, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H.sapiens]//2.4e-98:467:98//Hs.86337:AA149311

35 R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642

R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:H12594

40 R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259:61//Hs.76460:U49082

R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:D38081

45 R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512

R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345

50 R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355

55 R-NT2RP2003125

R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986

EP 1 074 617 A2

R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506

5 R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379

R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067

10 R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952

R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156

15 R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816

R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074

20 R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253

R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661

25 R-NT2RP2003243//ESTs//3.6e-53:300:92//Rs.18793:AA192438

R-NT2RP2003265//ESTs, Highly similar to protein NGD5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937

30 R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859

35 R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565:95//Hs.154919:AB014525

R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427

40 R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106

R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087

45 R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//Hs.1087:L20321

50 R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874

R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126

55 R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948

EP 1 074 617 A2

R-NT2RP2003339//ESTs//1.3e-85:441:96//Rs.24115:N32618

R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825

5 R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014

R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476

10 R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502

R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249

15 R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683

R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA
SUBUNIT [Canis familiaris]//1.2e-106:508:98//Hs.131840:AI016073

20 R-NT2RP2003445//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//5.6e-21:161:70//Hs.43153:N22360

25 R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [C.elegans]//6.0e-105:529:96//Hs.8055:
W60903

30 R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332

R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121

35 R-NT2RP2003499//ESTs, Weakly similar to elastin like protein [D.melanogaster]//7.0e-71:
365:95//Hs.101056:R52777

R-NT2RP2003506//ESTs, Weakly similar to ORF YPL207w [S.cerevisiae]//2.3e-115:577:
40 96//Hs.16277:N36831

R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733

45 R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:
94//Hs.78482:Y16270

R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-
50 sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:M12783

R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170

55 R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101

R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684

EP 1 074 617 A2

- 5 R-NT2RP2003559//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//1.8e-58:316:94//Hs.28891:W72439
- R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696
- 10 R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719
- R-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//4.7e-101:
495:98//Hs.34627:AA126463
- 15 R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete
cds//1.7e-103:501:97//Hs.58488:U97067
- R-NT2RP2003629//EST//0.032:440:59//Hs.135297:AI038981
- 20 R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN MURZ-
RPON INTERGENIC REGION [E.coli]//9.1e-62:359:92//Hs.12492:AA203188
- 25 R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951
- R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523
- 30 R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [C.elegans]//1.0:202:62//Hs.65539:
AI148540
- R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.3e-
35 99:492:96//Hs.93332:AA811920
- R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246
- 40 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4e-47:265:
93//Hs.78494:AB011097
- R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401
- 45 R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003
- R-nnnnnnnnnnnnn//Human 19.8 kDa protein mRNA, complete cds//0.84:221:60//Hs.2384:
50 U18914
- R-NT2RP2003737//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD
[Caenorhabditis elegans]//2.4e-50:302:90//Hs.19196:W74577
- 55 R-NT2RP2003751

EP 1 074 617 A2

R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808

R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709

5 R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606

R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds//6.0e-106:531:96//Hs.90436:AF047437

10 R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:AI381811

15 R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836

R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955

20 R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077

R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351:65//Hs.75196:X69838

25 R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124

R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167

30 R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341

R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:AI094611

35 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190:60//Hs.75875:U49278

R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568:97//Hs.35086:AB014458

40 R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540:97//Hs.7302:AB007916

45 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568:96//Hs.7316:AB018347

50 R-NT2RP2003984

R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087

55 R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519:99//Hs.36093:AI149968

EP 1 074 617 A2

R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:AI417478

R-NT2RP2004041

5 R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706

R-nnnnnnnnnnnnn//ESTs//1.4e-110:559:96//Hs.71916:AA219699

10 R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204

R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461

15 R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036

R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:AI147500

20 R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:AI342241

R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Anthocidaris
25 crassispina]//1.0e-118:583:97//Hs.16520:AI224533

R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:AI348544

30 R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:AA033974

R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589

35 R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167

R-NT2RP2004196

40 R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756

R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972

45 R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens]//5.2e-105:499:
98//Hs.143460:AA483305

R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116

50 R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds//3.4e-
103:530:93//Hs.54900:AF039687

55 R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483

R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744

EP 1 074 617 A2

R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187

5 R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056

R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//4.7e-110:544:96//Hs.61152:AF000416

10 R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788

R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223

15 R-NT2RP2004347

R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:AI268173

20 R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:AI129310

R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:AI218624

25 R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N32192

R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.4e-11:108:82//Hs.30490:AA146916

30 R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646

35 R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473

R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900

40 R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921

R-NT2RP2004412//ESTs//1.4e-105:503:98//Hs.15929:AA403121

45 R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:AI168124

R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N29695

50 R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDK1) mRNA, complete cds//8.6e-34:143:98//Hs.154729:AF017995

R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:AI270700

55 R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320

EP 1 074 617 A2

R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279:89//Hs.89887:D38081

5 R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:AI024347

R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470

10 R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:AI221661

R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126

15 R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666

R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862

20 R-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//4.5e-07:149:76//Hs.12845:N28835

R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497

25 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-118:587:96//Hs.5198:
AJ006291

30 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9e-107:520:
96//Hs.29956:AB007929

R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930

35 R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:M60858

R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0e-120:600:
96//Hs.154919:AB014525

40 R-NT2RP2004709//ESTs//1.1e-106:511:98//Hs.38034:AI149793

R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AA203433

45 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.3e-118:594:
96//Hs.4236:AB007947

50 R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015

R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423

55 R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774

R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013

EP 1 074 617 A2

- 5 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS)
mRNA, partial cds//8.0e-116:564:96//Hs.40820:AF058953
- R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579
- 10 R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//8.7e-120:584:
97//Hs.67052:AF054179
- R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:AI219906
- 15 R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803
- R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567
- 20 R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529
- R-nnnnnnnnnnn//ESTs//0.059:137:64//Hs.144109:AI345543
- 25 R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941
- R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:AI275458
- 30 R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506:
75//Hs.154326:D42087
- R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496
- 35 R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910
- R-NT2RP2004985
- 40 R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:AI419902
- R-NT2RP2005000
- 45 R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577:
95//Hs.155972:AB014515
- 50 R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235
- R-nnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:
97//Hs.31575:AF100141
- 55 R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161

EP 1 074 617 A2

R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507

R-NT2RP2005031//EST//3.1e-79:379:99//Hs.139709:AA227887

5 R-NT2RP2005037//ESTs//5.3e-102:551:93//Hs.26516:AA195220

R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:N49757

10 R-NT2RP2005108

R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518:97//Hs.22616:AB014564

15 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein) //4.6e-69:464:85//Hs.100555:X98743

20 R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383

R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180AI341261

25 R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:AI075744

R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438

30 R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:AI357582

R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648

35 R-NT2RP2005168//Homo sapiens mRNA for EIB-55kDa-associated protein//2.4e-101:513:95//Hs.155218:AJ007509

40 R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H.sapiens]//1.9e-115:577:96//Hs.7600:H98166

R-NT2RP2005227//Homo sapiens UM protein mRNA, complete cds//1.0e-45:359:82//Hs.154103:AF061258

45 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:245:97//Hs.21090:AA418587

50 R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503

R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412:95//Hs.23047:N66596

55 R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272

EP 1 074 617 A2

- R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:AI279001
- 5 R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete
cgs//2.4e-125:594:98//Hs.27007:AF060219
- 10 R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545:96//Hs.44766:
AJ007590
- R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:AI341261
- 15 R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338
- R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete
cgs//2.5e-45:272:91//Hs.1569:U11701
- 20 R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699
- 25 R-NT2RP2005 344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA,
complete cds//0.011:463:58//Hs.150926:AF017445
- R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:H14544
- 30 R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247
- R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:
82//Hs.93121:AB018304
- 35 R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces
cerevisiae]//2.5e-75:461:88//Hs.70849:AA121697
- 40 R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN
CHROMOSOME II [C.elegans]//8.1e-96:491:95//Hs.7194:AI185631
- 45 R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068
- R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:H14423
- 50 R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096
- R-NT2RP2005464//ESTs//1.8e-72:349:99//Hs.44045:N51307
- 55 R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:AI378936
- R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:AI222019

EP 1 074 617 A2

R-NT2RP2005476//ESTS//5.1 e-40:205:9811Hs.101577:AI168526

5 R-NT2RP2005490//ESTs//1.3e-70:364:96//Hs.134382:AA083573

R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455

10 R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540

R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426

15 R-NT2RP2005498//ESTS, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD
REGULATORY SUBUNIT, NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284:
88//Hs.85752:AI138993

20 R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755

R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C
IN CHROMOSOME I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071

25 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA,
complete cds//3.2e-110:570:9411Hs.119023:AF092563

30 R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
[H.sapiens]//1.3e-84:433:95//Hs.36942:AA524535

R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856

35 R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108:560:
94//Hs.159597:AJ012449

40 R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:
96//Hs.62515:AB007963

R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572

45 R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567

R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169

50 R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240

R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733

55 R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060

R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788

EP 1 074 617 A2

- R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229
- 5 R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211
- R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740
- 10 R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173
- R-NT2RP2005651//ESTS, Highly similar to XFIN PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:AA868470
- 15 R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302
- R-NT2RP2005669//Homo sapiens nitrilase 1 (VIII) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987
- 20 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91:434:98//Hs.25664:AF089814
- 25 R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229
- R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236
- 30 R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643
- R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos tauros]//2.8e-68:376:93//Hs.9095:AA532630
- 35 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638:AB018342
- 40 R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H.sapiens]//5.4e-105:500:98//Hs.14298:AI417523
- 45 R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982
- R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455
- 50 R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153
- R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258
- 55 R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064
- R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete

EP 1 074 617 A2

cds//4.3e-42:223:96//Hs.159651:AF068868

5 R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs.26285:AF082516

R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163

10 R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463

R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-112:559:96//Hs.14214:AI189379

15 R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs.22151:AI214321

20 R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664

R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724

25 R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398

R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746

30 R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981

R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122

35 R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403

R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062

40 R-NT2RP2005857//ESTs//1.0e-115:576:96//Hs.30663:AI338462

R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105

45 R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133

R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315

50 R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268

R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]//2.4e-73:397:94//Hs.16667:T92427

55 R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//2.8e-114:560:97//Hs.9082:AA873170

EP 1 074 617 A2

R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI338419

5 R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988

R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080

10 R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347

R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//1.2e-50:278:94//Hs.7194:AI185631

15 R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492

R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714

20 R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093

R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918

25 R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//Hs.46440:U21943

30 R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365

R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522

35 R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255:72//Hs.154103:AF061258

R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435

40 R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553:95//Hs.109299:AB014554

45 R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U79276

50 R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398

R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532:90//Hs.153910:X96484

55 R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312

EP 1 074 617 A2

R-NT2RP2006238//ESTs, Highly similar to rA8 [R.norvegicus]//1.5e-29:183:91//Hs.4048:AA404253

5 R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928

R-NT2RP2006261//ESTs//3.4e-57:3 26:92//Hs.22523:W02999

10 R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481:97//Hs.3404:AF035262

R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015

15

R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89:460:96//Hs.21889:N78664

20 R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771

R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412

25 R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321

R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411

30 R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:77//Hs.1361:M55053

35 R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.115325:D84488

R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092

40 R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146

R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595

45 R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs.72160:AJ006266

R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478

50

R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679

R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947

55

R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474

EP 1 074 617 A2

R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886

R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622

5 R-nnnnnnnnnnn//ESTs//2.0e-112:533:98//Hs.18685:AI393829

R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein
10 [M.musculus]//4.1e-109:542:97//Hs.7889:AI337112

R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:AI301598

15 R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:AJ011972

R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:
20 AF088219

R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213

25 R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:AI222202

R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI255095

30 R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574

R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029

35 R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA838715

R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI342241

40 R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000

R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:
45 96//Hs.13273:AB011164

R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418

50 R-NT2RP3000186

R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882

55 R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091

R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306

EP 1 074 617 A2

- R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N64817
- 5 R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819
- R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239
- 10 R-NT2RP3000251
- R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:532:97//Hs.111086:AI379177
- 15 R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073
- R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446
- 20 R-NT2RP3000299//ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]//3.6e-103:516:96//Hs.4894:AI191323
- 25 R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117
- R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438
- 30 R-NT2RP3000324
- R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267
- 35 R-NT2RP3000341//ESTs//0.51:251:61//Hs.94090:AA777689
- R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225
- 40 R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:556:96//Hs.111086:AI379177
- R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741
- 45 R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S.cerevisiae]//4.8e-91:439:97//Hs.31334:AI144423
- 50 R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI283303
- R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106
- 55 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:AF071185

EP 1 074 617 A2

R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947

R-NT2RP3000433

5 R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340

R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254

10 R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI379102

R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492

15 R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA
fragment//1.8e-23:347:70//Hs.114963:L34408

20 R-NT2RP3000484//Heparin cofactor II//0.98:166:62//Hs.1478:M58600

R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885141

25 R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X16667

R-NT2RP3000526//ESTs//1.6e-91:432:99//Hs.38042:AA187151

30 R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:AI078161

R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.95:85:
71//Hs.5184:AA709151

35 R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30180

R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:AI198036

40 R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:141:68//Hs.79077:
D87071

45 R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA779447

R-NT2RP3000582//ESTs//2.1 e-25:131:80//Hs.152465:AA563785

50 R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:AI241511

R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:AA953817

55 R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:AI190916

R-nnnnnnnnnnnn//Human mRNA for KIAA0314 gene, partial cds//1.5e-09:447:

EP 1 074 617 A2

58//Hs.155045:AB002312

- 5 R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA829880
- R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA422049
- 10 R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:AI127394
- R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]//5.4e-115:545:98//Hs.4857:AI090739
- 15 R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.3e-49:397:80//Hs.15519:AB018315
- 20 R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]//6.3e-92:434:99//Hs.152517:AA719022
- R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W27084
- 25 R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W76185
- R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81185
- 30 R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R60873
- R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.1465 89:AI085578
- 35 R-NT2RP3000736
- R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 [Rattus norvegicus]//1.8e-07:114:75//Hs.136065:W21960
- 40 R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:AI310447
- 45 R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA207243
- R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:AI378583
- 50 R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N20810
- R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582
- 55 R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:AI151081
- R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98082

EP 1 074 617 A2

R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA813022

5 R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154106:AI051657

R-NT2RP3000850

10 R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.79432:U03272

R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA576895

15 R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA505741

R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:N70837

20 R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:AI014673

R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84//Hs.75138:M88468

25 R-NT2RP3000901//ESTs//2.1e-95:466:97//Hs.10647:AA428217

R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA479385

30 R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus]//9.5e-113:566:96//Hs.5900:AA035728

R-NT2RP3000919

35 R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//1.5e-25:375:71//Hs.2953:X84407

R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA114178

40 R-NT2RP3000994//ESTs//3.5e 111:537:97//Hs.21146:AA683542

R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87405

45 R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:AI088029

R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA863044

50 R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]//5.6e-102:486:99//Hs.145956:AA007349

55 R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)//0.0012:447:58//Hs.2133:U18991

EP 1 074 617 A2

R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W87874

5 R-NT2RP3001096//ESTs//1.1e-110:540:96//Hs.42824:AA873182

R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832

10 R-nnnnnnnnnnnn//DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325

R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster]//3.2e-104:543:95//Hs.93796:C06063

15 R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575

R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878

20 R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779

R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180

25 R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166

R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188

30 R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761

R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305

35 R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//9.6e-113:552:97//Hs.23900:U82984

40 R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717

R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266

45 R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460

R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139

50 R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963

R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196

55 R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399

EP 1 074 617 A2

- R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588
- 5 R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048:AA524416
- 10 R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631
- R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997
- 15 R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135
- R-NT2RP3001268//Human Aac11(aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857
- 20 R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965
- R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.1113184:N25651
- 25 R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332
- R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691
- 30 R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571
- R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989
- 35 R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534:U35234
- 40 R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586:AB007920
- R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653
- 45 R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798
- R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090
- 50 R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778
- R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP95 [R.norvegicus]//5.7e-92:522:90//Hs.96200:AA218942
- 55 R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375

R-NT2RP3001396//ESTS//3.7e-111:528:98//Hs.22612:AA152232

5 R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628

R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186

10 R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898

R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817

15 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158

R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692

20 R-ntnnnnnnnnnnnn//Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397

R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374

25 R-NT2RP3001447//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.1e-101:482:98//Hs.124135:AA910560

30 R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994

R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219

35 R-NT2RP3001457//ESTS//1.5e-52:256:99//Hs.117982:AA644658

R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280

40 R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009

R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783

45 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395

50 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//6.8e-112:549:9711Hs.28285:AF064801

R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047

55 R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750

EP 1 074 617 A2

- R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463
- 5 R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:AA524416
- R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477
- 10 R-NT2RP3001587//Homo sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337
- 15 R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194
- R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328
- 20 R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798
- R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598
- 25 R-NT2RP3001629
- R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149
- 30 R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989
- R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709
- 35 R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030
- R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189
- 40 R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648
- R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225
- 45 R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558
- R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390
- 50 R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312
- 55 R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618
- R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669

EP 1 074 617 A2

- 5 R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1
PRECURSOR [Mus musculus]//4.1e-80:444:91//Hs.6823:W18181
- R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422099
- 10 R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923
- R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810
- 15 R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA740440
- R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968
- 20 R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H.sapiens]//1.2e-
87:450:96//Hs.20281:N92517
- R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725
- 25 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:
97//Hs.28169:AB007928
- 30 R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:
99//Hs.44268:AA455900
- R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X75962
- 35 R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292
- R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117
- 40 R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900
- R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792
- 45 R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642
- R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180
- 50 R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666
- 55 R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:
202:100//Hs.24709:AI123300
- R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781

R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737

R-NT2RP3001938//ESTs, Highly similar to SPORULATION-SPECIFIC PROTEIN 1
5 [Saccharomyces cerevisiae]//1.3e-95:483:96//Hs.5771:W74591

R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA160990

R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:AI291325

R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:AI025889

R-NT2RP3001989//ESTS, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310:99//Hs.11449:
15 AI201540

R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA897088

R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335:82//Hs.75087:X86779

R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA846729

R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291:89//Hs.155464:
25 AF088219

R-NT2RP3002033

R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W29081

R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426

R-NT2RP3002056//ESTs//1.4e-95:504:93//Hs.17428:AI365221

R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127:66//Hs.90438:
40 D63486

R-NT2RP3002062

R-nnnnnnnnnnnnn//ESTs//2.1e-113:552:97//Hs.9591:AA069657

R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:AA969139

R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N59148

R-NT2RP3002102

R-NT2RP3002108

EP 1 074 617 A2

- R-NT2RP3002146//ESTs//5.5e-58:296:97//Hs.65328:AA625385
- R-NT2RP3002147//EST//2.5e-53:387:81//Hs.147928:M249703
- 5 R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1
HOMOLOG [Homo sapiens]//6.2e-107:534:96//Hs.59523:AA602837
- 10 R-NT2RP3002163//ESTs//2.7e-106:520:97//Hs.21258:AA412293
- R-NT2RP3002165//ESTs//7.4e-93:479:95//Hs.27299:AI074024
- 15 R-NT2RP3002166//ESTs//1.0:261:59//Hs.132817:AA593713
- R-NT2RP3002173//ESTs//2.7e-93:512:92//Hs.23648:H07120
- 20 R-NT2RP3002181//ESTs//1.0e-84:435:96//Hs.47378:AI193598
- R-NT2RP3002244//ESTs//2.7e-11:97:89//Hs.9412:W72446
- 25 R-NT2RP3002248//ESTs//4.3e-90:459:95//Hs.9848:AA130588
- R-NT2RP3002255//ESTs//1.3e-45:289:88//Hs.9100:AA431672
- 30 R-NT2RP3002273//ESTs//2.3e-100:489:97//Hs.8258:AA744743
- R-NT2RP3002276//ESTs//1.2e-50:306:91//Hs.16160:AA778171
- 35 R-NT2RP3002303//ESTs//1.1e-67:323:99//Hs.129761:AA836898
- R-NT2RP3002304//ESTs//2.8e-86:405:99//Hs.29643:AA418500
- 40 R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1
HOMOLOG [H.sapiens]//1.8e-19:136:87//Hs.106928:AI041737
- R-NT2RP3002343//ESTs//1.0e-42:260:93//Hs.7797:W25667
- 45 R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221:
64//Hs.556:L41887
- 50 R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//5.8e-
105:516:94//Hs.6483:Y16355
- 55 R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524:
95//Hs.12707:AB014578
- R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108:

EP 1 074 617 A2

71//Hs.28914:Y00486

R-NT2RP3002501//ESTs//2.7e-96:489:95//Hs.27335:N74185

5

R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//3.2e-90:526:90//Hs.8083:AA521436

10

R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497:96//Hs.6650:AA843246

15

R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438:94//Hs.19542:AB018272

R-NT2RP3002549//ESTs//3.8e-98:493:96//Hs.7358:AA191673

20

R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.14:184:63//Hs.89230:AF031815

25

R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138:78//Hs.129883:AB007880

R-NT2RP3002590//ESTs//2.9e-51:290:93//Hs.162942:AI243850

30

R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58:100//Hs.76691:AF070673

35

R-NT2RP3002603

R-NT2RP3002631//ESTs//4.8e-54:367:85//Hs.13109:AA192514

40

R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA401365

R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA708573

45

R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA525172

R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [Drosophila melanogaster]//5.9e-109:537:97//Hs.19348:AA151678

50

R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA115502

R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA910871

55

R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-101:524:95//Hs.32580:AI123601

EP 1 074 617 A2

- R-NT2RP3002701//EST//0.87:131:63//Hs.161916:AA483169
- 5 R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA160945
- R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA809159
- 10 R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA526973
- R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:AI376958
- 15 R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71377
- R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA775240
- 20 R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:AI348080
- R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA909678
- 25 R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA019641
- R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA687262
- 30 R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//8.1e-14:146:72//Hs.129727:AF035587
- 35 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570:95//Hs.6162:AB018314
- R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:AI206286
- 40 R-NT2RP3002948//EST//1.0:102:65//Hs.144730:AI191975
- R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:AI201698
- 45 R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563:56//Hs.127338:AB007961
- 50 R-NT2RP3002969//ESTS, Weakly similar to LONG-CHAIN-FATTY-ACID-COA LIGASE 1 [Saccharomyces cerevisiae]112.0e-56:387:86//Hs.144597:W20143
- R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA476850
- 55 R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:AA252116
- R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:AI360553

EP 1 074 617 A2

R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA524423

5 R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN
[Mus musculus]//3.0e-100:528:94//Hs.90353:N98551

R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W05355

10 R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:AI141912

R-NT2RP3003068//ESTs, Weakly similar to M18.3 [C.elegans]//5.9e-83:392:99//Hs.101364:
15 AA534439

R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA180809

20 R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:AI359466

R-NT2RP3003101//EST//0.032:235:60//Hs.147920:AI202441

25 R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:AI003520

R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982

30 R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus
musculus]//3.3e-107:535:96//Hs.27437:AA004208

R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:AI271632

35 R-NT2RP3003150//ESTs//1.6e-99:539:91//Hs.46500:AA129774

R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007

40 R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:AI131226

R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944

45 R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796

R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:AI422634

50 R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573

R-NT2RP3003212//ESTs//1.8e-76:401:95//Hs.29067:N26107

55 R-NT2RP3003230//ESTs, Highly similar to CORONIN [Dictyostelium discoideum]//2.0e-40:
229:93//Hs.17377:AI078151

EP 1 074 617 A2

R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:AI290343

5 R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628

R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960

10 R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061

R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550:93//Hs.11702:L36983

15 R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:AI384035

R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055

20 R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818

R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:AI341261

25 R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:C05931

R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AA625445

30 R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:AI125289

R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs.112188:AA872993

35 R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102

R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:AI246155

40 R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567

R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272

45 R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721

R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.2e-24:418:67//Hs.139488:AI124095

50 R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372

55 R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041

R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023

EP 1 074 617 A2

- R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156
- 5 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479:96//Hs.14934:AF004828
- 10 R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527:93//Hs.26450:AB018268
- 15 R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106:549:94//Hs.7886:AI057529
- R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U02556
- 20 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)_n/(GTG)_n repeat-containing mRNA//4.1e-33:217:88//Hs.8068:U00952
- R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:AI123430
- 25 R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681
- R-NT2RP3003564
- 30 R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:N48721
- R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944
- 35 R-NT2RP3003589//EST//0.58:242:59//Hs.130804:AA894759
- R-NT2RP3003625//ESTs//7.6e-41:349:80//Hs.140608:N53448
- 40 R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222:60//Hs.17217:U49957
- 45 R-NT2RP3003659//ESTs//2.0e-113:547:97//Hs.23389:AA769310
- R-NT2RP3003665//ESTs//1.6e-80:415:95//Hs.141084:H11714
- 50 R-NT2RP3003672
- R-NT2RP3003686//ESTs//6.8e-114:552:97//Hs.43299:N23036
- 55 R-NT2RP3003701//ESTs//2.1e-16:282:66//Hs.115512:AI208768
- R-NT2RP3003716//ESTs//2.1e-45:195:91//Hs.41296:N71923

EP 1 074 617 A2

R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.6e-103:492:97//Hs.48513:AB018300

5 R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863

R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747

10 R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913

R-NT2RP3003800//PROTO-ONCOGENE TYRO SINE-PROTEIN KINASE SRC//8.9e-108:551:95//Hs.115742:AF077754

15

R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446

20 R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456:95//Hs.5555:AI285198

R-NT2RP3003819//Interleukin 10//3.3e-43:173:89//Hs.2180:M57627

25 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761

R-NT2RP3003828//ESTs, Weakly similar to unknown.[H.sapiens]//9.6e-98:511:95//Hs.26955:AI333224

30

R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743

35 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:AF070611

R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888

40 R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962

R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298

45 R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170

R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726

50 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933

R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221

55 R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409

R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593

EP 1 074 617 A2

R-NT2RP3 004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142

5 R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714

R-NT2RP3004041

10 R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820

R-NT2RP3004070//ESTs//5.5e-108:552:9511Hs.23392:AI310139

15 R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W4537

R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs.140932:AI262104

20 R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045

R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS
[C.elegans]//3.5e-76:402:95//Hs.55847:W31092

25 R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696

R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334

30 R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:AI183425

R-NT2RP3004155//ESTs//1.7e-110:558:96//Hs.27003:AI279093

35 R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila
melanogaster]//1.8e-40:200:100//Hs.26089:AA195126

40 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41:266:
89//Hs.6314:AA522619

R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL
45 HYDROLASE C13A11.04C [Schizosaccharomyces pombe]//3.7e-112:547:97//Hs.99819:
AI346680

R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794

50 R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:N46252

R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827

55 R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628

EP 1 074 617 A2

R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]//1.6e-89:468:95//Hs.5117:AA831530

5 R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:T87623

R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:AI273630

10 R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:AI200264

R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258

15

R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223

R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA863044

20

R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224

25 R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans]//0.30:253:58//Hs.97184:AA385934

R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985

30

R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621

R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349:AB007917

35

R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616

R-NT2RP3004470//EST//0.032:70:71//Hs.147925:AI249332

40

R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406

45 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521:97//Hs.5003:AB007925

R-NT2RP3004480

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R-NT2RP3004490//ESTs//4.7e-68:354:95//Hs.163721:H42504

R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]//3.4e-100:508:95//Hs.47393:AA218858

55

R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735

EP 1 074 617 A2

R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]/1.8e-83:465:92//Hs.137064:AA318257

5 R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:AI051971

R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:AI279865

10 R-nnnnnnnnnnnnn

R-NT2RP3004544//EST//0.035:226:60//Hs.99195:AA449232

15 R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461

R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674

20 R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:AI420493

R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456

25 R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:AI080213

R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157

30 R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723

R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds//7.2e-57:291:95//Hs.8786:AB014680

35

R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:AI123335

R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA418560

40

R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219

45 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289:82//Hs.51233:AF016266

50 R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens]/8.3e-98:462:99//Hs.10114:AI345945

R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030

55 R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287

R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:

96//Hs.57929:AB011538

R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554:
97//Hs.64691:AB007952

R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014

R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294

R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436

R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295

R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N66569

R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257

R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505:96//Hs.13999:AB014600

R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788

R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272:90//Hs.40100:
AB002390

R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185

R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.9e-70:
354:96//Hs.155481:AJ006470

R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757

R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379:99//Hs.43728:AF091092

R-NT2RP4000263

R-rrrrrrrrrrrrr/ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//4.7e-104;525:96//Hs.152069:AA548972

R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:AI271631

R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99//Hs.13410:AF070524

EP 1 074 617 A2

R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760

R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390

5

R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.6e-111:520:99//Hs.107479:AB018281

10

R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-110:527:98//Hs.31323:AF044195

R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:AI301130

15

R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA604498

R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376

20

R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//3.9e-87:499:91//Hs.26156:AA630975

25

R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-95:468:96//Hs.93871:AI191318

30

R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:AI189011

R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60955

35

R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:AI037953

R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.35:153:63//Hs.113286:U77783

40

R-nnnnnnnnnnnn//ESTs//4.5e-89:455:96//Hs.62638:AA127740

R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:AI204167

45

R-nnnnnnnnnnnn

R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [C.elegans]//1.2e-40:125:97//Hs.56124:AI424792

50

R-NT2RP4000515//EST//6.7e-30:183:90//Hs.150710:AI122713

55

R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:183:76//Hs.83155:U10868

R-NT2RP4000518//EST//0.091:178:58//Hs.133031:AI049874

EP 1 074 617 A2

R-NT2RP4000519

5 R-NT2RP4000524//ESTS, Highly similar to rsec8 [R.norvegicus]//3.4e-93:496:93//Hs.107394:
H07126

10 R-NT2RP4000528//EST//0.84:130:66//Hs.140208:AA702213

R-NT2RP4000541//EST//5.2e-63:337:94//Hs.156337:AI337328

15 R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11
[R.norvegicus]//8.2e-92:448:98//Hs.25597:H93026

R-NT2RP4000588//ESTs//3.8e-94:445:98//Hs.44077:N28840

20 R-NT2RP4000614//ESTs//6.5e-18:159:83//Hs.24549:N57263

R-NT2RP4000638//ESTs//2.5e-46:296:87//Hs.132722:AA618531

25 R-NT2RP4000648//ESTs//2.6e-103:559:93//Hs.23794:W80393

R-NT2RP4000657//ESTs//1.0:189:60//Hs.87073:AA972704

30 R-NT2RP4000704//ESTs//2.8e-101:509:96//Hs.84824:AA935651

R-NT2RP4000724//ESTS//1.5e-83:442:94//Hs.142114:AA205615

35 R-NT2RP4000728//ESTs//0.84:61:75//Hs.145334:AI251399

R-NT2RP4000739//ESTs//8.8e-80:418:94//Hs.42959:N21211

40 R-NT2RP4000781//ESTs//1.4e-79:376:99//Hs.135458:AI081312

R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//3.1e-106:550:
45 94//Hs.25132:AB007939

R-NT2RP4000833//ESTs//5.8e-46:309:85//Hs.163979:AA828834

50 R-NT2RP4000837//ESTs//1.7e-112:539:97//Hs.97718:AI334028

R-NT2RP4000855//ESTs//1.1e-95:486:95//Hs.5345:AA988104

55 R-NT2RP4000865//EST//6.2e-68:412:89//Hs.142196:AA258356

R-NT2RP4000878//ESTs//1.9e-80:417:95//Hs.104716:AI023185

EP 1 074 617 A2

R-NT2RP4000879//ESTs//1.8e-42:211:99//Hs.89991:AI374617

R-nnnnnnnnnnn//ESTs//1.2e-89:453:97//Hs.100182:N92594

5 R-nnnnnnnnnnn//EST//9.4e-06:197:63//Hs.145970:AI277106

R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [H.sapiens]//5.9e-17:134:
10 85//Hs.14146:W92235

R-nnnnnnnnnnn//ESTs//4.3e-14:84:100//Hs.155360:AA984683

15 R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial
cds//8.2e-108:548:95//Hs.24812:AF069532

R-NT2RP4000929//ESTs//1.3e-119:567:98//Hs.62717:AA044905

20 R-NT2RP4000955//ESTs//3.5e-10:1 19:78//Hs.42946:N21111

R-NT2RP4000973//ESTs//2.8e-05:93:69//Hs.155126:AA563986

25 R-NT2RP4000975//ESTs//4.4e-58:324:95//Hs.126070:AA045179

R-NT2RP4000979//ESTs//3.5e-42:468:73//Hs.106210:AI193017

30 R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence//8.7e-120:570:
98//Hs.12457:AF052123

35 R-NT2RP4000989//ESTs//1.3e-122:581:98//Hs.10499:AA528018

R-NT2RP4000996//ESTs//9.2e-113:579:94//Hs.23762:N26620

40 R-NT2RP4000997//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete
cds//1.1e-28:439:68//Hs.129735:AF010144

R-NT2RP4001004//ESTs//3.6e-78:389:98//Hs.156290:AI016769

45 R-NT2RP4001006//ESTS, Moderately similar to ORF2: function unknown [H.sapiens]//6.6e-
124:574:99//Hs.47393:AA218858

50 R-NT2RP4001010//EST//2.8e-31:194:90//Hs.161186:AI418635

R-NT2RP4001029//ESTs//4.4e-111:523:99//Hs.28423:AI336292

55 R-NT2RP4001041//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC
[Saccharomyces cerevisiae]//3.6e-114:569:96//Hs.6762:AA088424

EP 1 074 617 A2

R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282:94//Hs.100955:AB007859

5 R-NT2RP4001064//ESTs, Weakly similar to protein B [H.sapiens]//2.1e-103:485:99//Hs.10114:AD45945

R-NT2RP4001078

10

R-NT2RP4001079//Homo sapiens mRNA for putative Ca^{2+} -transporting ATPase, partial//1.7e-119:569:98//Hs.106778:AJ010953

15

R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548:95//Hs.13273:AB011164

20

R-NT2RP4001095//ESTs//1.5e-113:563:96//Hs.118732:AI344055

R-NT2RP4001100//ESTs//2.0e-46:413:79//Hs.146314:R99617

25

R-NT2RP4001117//EST//7.4e-51:294:92//Hs.7260:T23737

R-NT2RP4001122//ESTs//5.4e-109:509:99//Hs.16390:AI052357

30

R-NT2RP4001126//EST//0.97:169:61//Hs.148107:AA693476

R-NT2RP4001138//ESTs//3.0e-110:543:97//Hs.57655:AI056890

35

R-NT2RP4001143//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//5.4e-113:573:96//Hs.5249:U55977

40

R-NT2RP4001148//ESTs//3.1e-103:490:98//Hs.121282:AI091453

R-NT2RP4001149//EST//1.7e-50:281:93//Hs.101727:H16171

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R-NT2RP4001150//ESTs//1.9e-90:422:100//Hs.125490:AI138884

R-NT2RP4001159

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R-NT2RP4001174//ESTs//2.5e-110:526:98//Hs.116555:AA639278

R-nnnnnnnnnnnnn//ESTs//1.1 e-25:140:97//Hs.83756:AI002822

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R-NT2RP4001207//ESTs//4.4e-70:432:89//Hs.13109:AA192514

EP 1 074 617 A2

R-NT2RP4001210//ESTs//1.4e-108:509:99//Hs.27021:AI359495

5 R-NT2RP4001213//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//4.4e-123:624:95//Hs.22744:AI379892

R-NT2RP4001219//ESTs//0.0043:142:65//Hs.6733:AI160750

10 R-NT2RP4001228//ESTs//4.9e-101:482:98//Hs.62684:AA806103

R-NT2RP4001235//ESTs//3.7e-105:571:93//Hs.37706:AA005120

15 R-NT2RP4001256//ESTs//1.1e-12:189:74//Hs.20621:W28255

R-NT2RP4001260//EST//6.9e-05:313:61//Hs.116438:AA648430

20 R-NT2RP4001274//EST//0.0020:246:63//Hs.149955:AI289933

R-nnnnnnnnnnnn//ESTs//2.9e-34:213:91//Hs.43100:AA186588

25 R-NT2RP4001313

R-NT2RP4001315//EST//6.1e-38:217:93//Hs.97832:AA400892

30 R-NT2RP4001339//ESTs//3.8e-91:430:99//Hs.34840:AI279612

R-NT2RP4001345//ESTs//5.3e-89:443:96//Hs.6770:AA972732

35 R-NT2RP4001351//ESTs//6.0e-78:394:97//Hs.102796:N70837

R-NT2RP4001353//ESTs//4.8e-06:90:82//Hs.7778:AA195616

40 R-NT2RP4001372

R-NT2RP4001373//ESTs, Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC REGION [Saccharomyces cerevisiae]//1.7e-108:546:96//Hs.32271:AA203680

45 R-NT2RP4001375//ESTs//2.4e-19:155:87//Hs.62119:AA043299

50 R-NT2RP4001379//EST//4.4e-29:288:72//Hs.157848:AI362501

R-NT2RP4001389//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.8e-79:438:93//HS.21938:W81045

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EP 1 074 617 A2

R-NT2RP4001407//ESTs//8.3e-112:541:97//Hs.22587:AA743132

R-NT2RP4001414//ESTs//8.6e-18:117:90//Hs.90789:W27649

5 R-NT2RP4001433//ESTs, Moderately similar to PROHIBITIN [H.sapiens]//1.6e-102:498:97//Hs.62386:AA512948

10 R-NT2RP4001442//ESTs//8.8e-104:489:99//Hs.101619:AI339433

R-NT2RP4001447

15 R-NT2RP4001474

R-NT2RP4001483//ESTs//2.1e-100:528:92//Hs.17860:AA706655

20 R-NT2RP4001498//ESTs//1.1e-97:470:98//Hs.95744:AI392846

R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93511

25 R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA625385

R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//2.9e-107:546:96//Hs.5570:AI377863

30 R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:AI336292

R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium tetraurelia]//2.8e-120:566:98//Hs.108530:AA523928

35 R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium tetraurelia]//2.8e-120:566:98//Hs.108530:AA523928

R-NT2RP4001547//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26:184:88//Hs.136189:AA133224

40 R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:AA677552

R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:AA292285

45 R-NT2RP4001568//ESTs//6.4e-55:300:94//Hs.57442:N63437

R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA521251

50 R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA225906

R-NT2RP4001575

55 R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL[S.cerevisiae]//8.7e-112:557:97//Hs.7558:AA526812

EP 1 074 617 A2

- R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA166776
- 5 R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA069657
- R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA534737
- 10 R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e-116:559:97//Hs.5332:AF007151
- R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H.sapiens]//5.3e-36:192:97//Hs.5662:AA868361
- 15 R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II [Caenorhabditis elegans]//1.1e-104:525:96//Hs.20472:W28734
- 20 R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805
- R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118:583:96//Hs.15562:U96629
- 25 R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:N25941
- 30 R-ntntntntntntntntntnt//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//3.4e-73:362:97//Hs.152332:AI141922
- 35 R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692
- R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:X78926
- 40 R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315
- R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62:326:94//Hs.110839:W28098
- 45 R-NT2RP4001803
- R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:AI161133
- 50 R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:AI218434
- R-NT2RP4001828//ESTs//3.3e-101:536:92//Hs.18851:AA857826
- 55 R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663

EP 1 074 617 A2

R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210

5 R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:88//Hs.154326:D42087

R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602

10 R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:AI345528

R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:AI018606

15 R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:AI417099

R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848

20 R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436

R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:AI341793

25 R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310:82//Hs.73919:X81637

R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//8.3e-87:457:94//Hs.41793:AA775879

30 R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252

R-NT2RP4002018

35 R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//4.7e-09:90:86//Hs.41127:AA555184

40 R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738

R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106

45 R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679

R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198

50 R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464:82//Hs.144228:N99507

55 R-ntnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271:100//Hs.6185:AA428565

R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407

EP 1 074 617 A2

R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592

5 R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555

R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//1.9e-65:373:92//Hs.31532:H18272

10 R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090

R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605:94//Hs.108258:AB007934

15 R-OVARC1000004

R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929

20 R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635

R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273

25 R-OVARC1000017

R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI078286

30 R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331:83//Hs.96247:X95073

35 R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041

R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367

40 R-OVARC1000071//ESTs//2.5e-60:321:96//Us.25010:R6787

R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:AL031259

45 R-nnnnnnnnnnnnn//ESTs//1.0e-111:526:98//Hs.129020:AI380703

R-OVARC1000091//ESTS, Weakly similar to HOST CELL FACTOR CI [H.sapiens]//3.9e-112:596:94//Hs.20597:W58370

50 R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:AI289942

55 R-OVARC1000106

R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA,

EP 1 074 617 A2

complete cds//8.3e-102:495:97//Hs.3688:AF069250

5 R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489:74//Hs.101238:Y11312

R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482

10 R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:AI333214

R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090

15 R-OVARC1000151

R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023

20 R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629

R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339:81//Hs.154103:AF061258

25 R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196:92//Hs.64322:AA142864

30 R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874

R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958

35 R-OVARC1000241//EST//0.00018:115:68//Hs.150728:AI123130

R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403:93//Hs.108117:AI097079

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R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476

45 R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-37:191:98//Hs.20725:AI027777

R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449

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R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743

55 R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//1.3e-98:488:96//Hs.125749:AI377682

R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:AI050863

EP 1 074 617 A2

R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672

5 R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423

R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928

10 R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219

R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27:211:79//Hs.108287:L27670

15 R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237

R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034

20 R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:AI123426

R-OVARC1000437

25 R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:AI018671

R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45:320:84//Hs.73614:U83460

30 R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79:418:94//Hs.12334:AB014583

35 R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582

R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576

40 R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:AI421211

R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926

45 R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102:514:96//Hs.11833:AI299947

50 R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983

R-OVARC1000496

55 R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484

R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:87//Hs.155464:

EP 1 074 617 A2

AF088219

5 R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48:264:92//Hs.49860:AA702248

R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021

10 R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:202:85//Hs.90859:X85106

15 R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:AI244285

R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:AI141587

20 R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627

R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:84//Hs.155464:AF088219

25 R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053

R-OVARC1000605

30 R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47:417:77//Hs.159897:AB007970

35 R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28:366:72//Hs.96247:X95073

40 R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31:162:100//Hs.111862:AB011162

R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480

45 R-nnnnnnnnnnnnn//ESTs//0.94:416:59//Hs.130754:AA279522

R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:AI032875

50 R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.053:160:64//Hs.108447:AJ000517

55 R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:141:73//Hs.32511:AB007901

R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461

EP 1 074 617 A2

R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:AI141736

5 R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918

R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-28:430:69//Hs.42457:AA523306

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R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016

R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793

15

R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659

R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19:119:95//Hs.3069:L11066

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R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:AI419764

25 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106:536:95//Hs.61628:Y17711

R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87//Hs.73919:X81637

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R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:579:96//Hs.18910:AF045584

35 R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096

R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:AI150674

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R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:AI336292

R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENIC REGION [Bacillus subtilis]//7.9e-98:525:93//Hs.10366:W21953

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R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777

R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401

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R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350

R-OVARC1000912

55

R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814

EP 1 074 617 A2

R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127

R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696

5 R-OVARC1000937//EST//1.1e-53:290:95 //Hs.162846:AA631215

R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794

10 R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971

R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs.155464:
15 AF088219

R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:
20 AL022394

R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909

R-OVARC1000984//ESTS, Weakly similar to No definition line found [C.elegans]//3.5e-68:
25 346:96//Hs.25544:AA532784

R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811

30 R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:
AB007874

R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:N53448

35 R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.7e-28:181:
77//Hs.139107:K00629

40 R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270

R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117

45 R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630

R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA,
complete cds//2.1e-09:137:74//Hs.77579:AF013263

50 R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:501:
96//Hs.9899:AF099149

55 R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046

R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:N94384

EP 1 074 617 A2

- R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962
- 5 R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231
- R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:N98652
- 10 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:AF082657
- R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844
- 15 R-OVARC1001074
- R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U57029
- 20 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897
- 25 R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//3.3e-75:386:95//Hs.26584:AF051782
- 30 R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds//3.9e-37:283:84//Hs.46468:U45984
- 35 R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548
- R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312
- 40 R-OVARC1001161//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//2.2e-66:346:95//Hs.53263:AA173226
- R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223
- 45 R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727
- R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200
- 50 R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs.155464:AF088219
- 55 R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223
- R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA,

EP 1 074 617 A2

complete cds//6.6e-64:247:80//Hs.97203:U83171

- 5 R-OVARC1001188//ESTs//4.1e-18:296:69//Hs.139197:AA228343
- R-OVARC1001200//ESTs//2.0e-28:207:85//Hs.35121:AA877826
- 10 R-OVARC1001232//ESTs//3.2e-61:358:91//Hs.6449:W95025
- R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668
- 15 R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361
- R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344166
- 20 R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929
- R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708
- 25 R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532
- R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:AI263113
- 30 R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885
- R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334:100//Hs.23763:AB011090
- 35 R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304:83//Hs.73919:X81637
- R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1.0:147:63//Hs.76494:U41344
- 40 R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:76//Hs.155464:AF088219
- 45 R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//6.9e-85:464:93//Hs.23651:AA650356
- R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67247
- 50 R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216
- R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90657
- 55 R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844

EP 1 074 617 A2

R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777

R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415

5 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344:72//Hs.153468:AB011147

10 R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958

R-OVARC1001391

15 R-nnnnnnnnnnnr//ESTs//0.003 9:48:95//Hs.117964:N20913

R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561:95//Hs.21586:AB006651

20 R-OVARC1001419

R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136

25 R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427

R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345

30 R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592

R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700

35 R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694

R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089

40 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585:96//Hs.6534:AF016507

45 R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:90//Hs.155464:AF088219

R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539

50 R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566:95//Hs.6396:AB016492

55 R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388

R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA7/4.4e-20:

EP 1 074 617 A2

150:89//Hs.155160:AF031166

5 R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:72//Hs.154326:D42087

R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:N32019

10 R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965

R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78//Hs.5158:AB007869

15 R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659

R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854

20 R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080

R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784

25 R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]//1.2e-27:236:81//Hs.15485:AA046954

30 R-OVARC1001731//Tropomyosin4(fibroblast)//7.9e-74:422:90//Hs.102824:X05276

R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.7e-62:300:83//Hs.144563:AF057280

35 R-nnnnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//6.8e-100:540:92//Hs.117741:AA903456

40 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.1e-109:567:94//Hs.155377:U97670

45 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529:97//Hs.15869:AB014575

R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127

50 R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604

R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978

55 R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81//Hs.153563:AF011333

EP 1 074 617 A2

R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688

R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831

5 R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519:63//Hs.25639:AB011110

10 R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705

R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621

15 R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160

R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809

20 R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence/1.9e-105:571:91//Hs.25300:AF070611

R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476

25 R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302:90//Hs.153468:AB011147

30 R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310

R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//1.6e-87:346:90//Hs.6216:AF061749

35 R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435

R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855

40 R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842

R-OVARC1001928

45 R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:253:88//Hs.117741:AA903456

50 R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637

R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.22744:AI379892

55 R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875

EP 1 074 617 A2

- R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729
- R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887
- 5 R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA618531
- R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:AB007934
- 10 R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI088556
- R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:AB018315
- 15 R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860
- 20 R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130
- R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.7e-102:485:98//Hs.137516:AA805691
- 25 R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825
- R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923
- 30 R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631
- R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160
- 35 R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478
- R-PLACE1000004//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//7.5e-32:164:99//Hs.144194:AA706337
- 40 R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920
- 45 R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557
- R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223
- 50 R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870
- R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:AI310440
- 55 R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:

EP 1 074 617 A2

86//Hs.23094:M19503

R-PLACE100005011ESTs//9.7e-90:453:96//Hs.27410:N25612

5

R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499

R-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3
[C.elegans]//1.4e-61:331:94//Hs.30026:AI356771

10

R-PLACE1000078//ESTs//2.6e-30:212:85//Hs.89312:AA167659

15

R-PLACE1000081

R-PLACE1000094

20

R-PLACE1000133//ESTs//4.4e-87:448:94//Hs.93748:AA884505

R-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//5.5e-103:538:
94//Hs.9670:AA632135

25

R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete
cds//4.1e-114:594:94//Hs.151017:AF058291

30

R-PLACE1000185//ESTs, Weakly similar to No definition line found [C.elegans]//2.0e-19:114:
95//Hs.7036:W22072

R-PLACE1000213//ESTs//9.4e-99:494:96//Hs.24398:AI262946

35

R-PLACE1000214//ESTs//5.3e-98:466:98//Hs.28661:AA805916

R-PLACE1000236//Human BENE mRNA, partial cds//1.7e-19:162:84//Hs.85889:U17077

40

R-PLACE1000246//EST//0.026:134:66//Hs.135611:Z21545

R-PLACE1000292//ESTs//2.5e-80:418:96//Hs.138233:N57912

45

R-PLACE1000332//EST//1.7e-82:422:96//Hs.118637:T61940

R-PLACE1000347//ESTs//8.5e-36:180:100//Hs.6377:AA632424

50

R-PLACE1000374//ESTs//2.8e-90:434:98//Hs.161785:AI423126

R-PLACE1000380//ESTs//1.0e-81:399:97//Hs.47105:AI334994

55

R-PLACE1000383//ESTs//3.7e-75:405:94//Hs.23200:AA203708

EP 1 074 617 A2

R-PLACE1000401//ESTs//1.4e-16:212:72//Hs.151665:AA020959

5 R-PLACE1000406//ESTs//2.1e-51:259:97//Hs.129651:N53089

R-PLACE1000420//ESTs//7.7e-92:471:95//Hs.144407:AA737799

10 R-PLACE1000421//ESTs//2.9e-14:282:67//Hs.142068:AA176125

R-PLACE1000424//EST//2.9e-35:453:70//Hs.162404:AA573131

15 R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.6e-47:472:77//Hs.113259:AF023456

R-PLACE1000444//ESTs, Moderately similar to platelet glycoprotein IIb precursor [H.sapiens]//2.0e-58:410:81//Hs.97579:AA398118

20 R-PLACE1000453//ESTs//2.3e-85:442:95//Hs.9725:AA039793

R-PLACE1000481//ESTS, Weakly similar to Ndr protein kinase [H.sapiens]//3.2e-109:549:95//Hs.19074:U69566

25 R-PLACE1000492//ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [R.norvegicus]//3.5e-83:435:94//Hs.26510:AA700425

30 R-PLACE1000540//ESTs//3.2e-58:281:99//Hs.118270:AA844729

R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.2e-32:208:88//Hs.153026:AB014540

35 R-PLACE1000562//ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN IXR1-TFA1 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-26:220:81//Hs.163791:W25348

40 R-PLACE1000564//ESTs//1.1e-54:302:92//Hs.158520:AI380485

R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404:75//Hs.153014:AB002353

45 R-nnnnnnnnnnnn//Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82//Hs.62661:M55542

50 R-PLACE1000596//ESTs//0.0028:364:59//Hs.106090:AA457030

R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds//4.3e-49:295:90//Hs.154326:D42087

55 R-PLACE1000610//ESTs//0.0010:104:74//Hs.17413:N45301

EP 1 074 617 A2

- R-PLACE1000636//ESTs//1.8e-64:340:95//Hs.100895:AA479308
- 5 R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:96//Hs.5819:AF102265
- 10 R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//1.4e-102:559:92//Hs.29595:AJ005896
- 15 R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:64//Hs.128763:AF009353
- R-PLACE1000712//ESTs//7.8e-60:317:95//Hs.8245:AA115485
- 20 R-PLACE1000716
- R-PLACE1000748//ESTs//8.9e-87:466:93//Hs.25245:AA176701
- 25 R-PLACE1000749//EST//0.019:186:61//Hs.135443:AI077396
- R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE . K12H4.8 IN CHROMOSOME III [C.elegans]//3.9e-40:224:94//Hs.87889:AA262008
- 30 R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536
- 35 R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:AB014548
- R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482
- 40 R-nnnnnnnnnnnn//H.sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.20144:AF088219
- 45 R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189
- R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]//7.7e-31:220:86//Hs.117576:R33135
- 50 R-nnnnnnnnnnnn//ESTs//1.8e-87:459:94//Hs.43100:AA186588
- R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:AI275039
- 55 R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces cerevisiae]//2.2e-92:467:95//Hs.6118.-AI141558

EP 1 074 617 A2

R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:AI392846

5 R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:AI097091

R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697

10 R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:AI002941

R-PLACE1000977//EST//0.085:153:65//Hs.131646:AI025689

15 R-PLACE1000979

R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725

20 R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens]//5.2e-63:343:93//Hs.5662:AA868361

R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146

25 R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878

R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736

30 R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:AI025762

R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120

35 R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124

R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580

40 R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259:59//Hs.31575:AF100141

45 R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268

R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610

50 R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594

R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834

55 R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]//0.91:77:71//Hs.115211:AA287527

R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297

EP 1 074 617 A2

- 5 R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor
[M.musculus]//1.9e-99:512:94//Hs.24884:AA176812
- R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:AI073464
- 10 R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131
- R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371
- 15 R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780
- R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:AI334460
- 20 R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN
GEG-154 [M.musculus]//2.7e-22:181:84//Hs.48320:AA149548
- R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]//4.2e-
34:195:92//Hs.86276:W27601
- 25 R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:AI339056
- R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete
30 cds//5.5e-44:215:86//Hs.50984:U01160
- R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:AI097077
- 35 R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:
AF088219
- R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:
40 93//Hs.152005:AF009615
- R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence/1.0e-36:192:97//Hs.12342:
45 AF055030
- R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA,
complete cds//1.0e-86:456:94//Hs.21301:AF093419
- 50 R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:AI298280
- R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555
- 55 R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348
- R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:

EP 1 074 617 A2

242:95//Hs.110404:AF091087

- 5 R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800
- R-PLACE1001440
- 10 R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115.
- R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AI017547
- 15 R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:AI248625
- R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617
- 20 R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361
- R-PLACE1001517//Homo sapiens hGAAl mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969
- 25 R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153
- R-PLACE1001545/TESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//1.6e-22:170:85//Hs.155456:AA707265
- 30 R-PLACE1001551//ESTs//1.5e-39:202:98// Hs.139269:AA894431
- R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249
- 35 R-PLACE1001602//EST//0.33:297:57//Hs.149839:AI287601
- R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904
- 40 R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683
- R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:AF054174
- 45 R-PLACE1001632//ESTs,*Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.114547:AA167095
- 50 R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:AI168526
- R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640
- 55 R-PLACE10016727/ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!
[H.sapiens]//0.98:141:62//Hs.153060:AA195804

EP 1 074 617 A2

- 5 R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-113:545:97//Hs.3688:AF069250
- R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124
- 10 R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:AI374903
- R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667
- 15 R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993
- R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171
- 20 R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113
- R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266
- 25 R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479
- R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI423937
- 30 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:AF061243
- 35 R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662
- R-PLACE1001761
- 40 R-PLACE1001771//ESTs//0.92:165:62//Hs.473 87:N51980
- R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236
- 45 R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352
- R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA; partial cds//1.3e-93:463:95//Hs.40820:AF058953
- 50 R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219
- 55 R-PLACE1001845
- R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868

EP 1 074 617 A2

R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009

R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098

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R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:AF099936

10

R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130:66//Hs.151406:AB014523

R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313

15

R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941

R-PLACE1002046

20

R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595

R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094

25

R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619

R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:AI028552

30

R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA731632

R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311

35

R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293

R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937

40

R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:AI167614

R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE
HOMOLOG[H.sapiens]//3.6e-39:400:76//Hs.162172:AA534189

45

R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:AI185965

50

R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745

R-PLACE1002205//ESTs//1.5e-39:211:95//Hs.28338:N48793

55

R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788

R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892

EP 1 074 617 A2

- R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:AI004257
- 5 R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8e-67:501:81//Hs.23094:M19503
- R-PLACE1002319//ESTs//1.4e-28:17 8:92//Hs.7353:AA209308
- 10 R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501:93//Hs.18277:AB018271
- 15 R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291
- R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381
- 20 R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959
- R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110
- 25 R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804
- R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333
- 30 R-PLACE1002465//ESTs//1.6e-92:488:93//Hs.78110:AA741320
- R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166:85//Hs.19368:U69263
- 35 R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132
- 40 R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273
- R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429
- 45 R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83//Hs.5158:AB007869
- 50 R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!
[H.sapiens]//6.4e-14:217:69//Hs.152230:AI140609
- R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582:85//Hs.88756:AB018256
- 55 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116:

EP 1 074 617 A2

93//Hs.99348:AC004774

R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491

5

R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437

10

R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131

R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:AI339738

15

R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778

R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]//1.2e-44:228:97//Hs.7527:AA843208

20

R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147

R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749

25

R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130

30

R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180

R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830

35

R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445:90//Hs.29202:R71586

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R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:H12865

R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:AI334099

45

R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:AI149014

R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593

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R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955

R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392

55

R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916

R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-

EP 1 074 617 A2

42:233:94//Hs.61518:AA167094

- 5 R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142
- R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756
- 10 R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539
- R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762
- 15 R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332
- R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995
- 20 R-PLACE1002962
- R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202
- R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941
- 25 R-PLACE10029937/ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!
[H.sapiens]//1.3e-86:502:89//Hs.32232:AA604268
- 30 R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268
- R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499
- 35 R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156r60//Hs.82042:
D87075
- 40 R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:
200:63//Hs.214:U04840
- R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777
- 45 R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium
melliloti]//9.5e-94:491:93//Hs.6318:AI131178
- 50 R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359
- R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:
U51920
- 55 R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757
- R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467

EP 1 074 617 A2

R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924

5 R-PLACE1003176

R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453

10 R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017

R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802

15 R-PLACE100323 8//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W79123

R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//Hs.73614:U83460

20 R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131

25 R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:551:92//Hs.52431:AA625326

R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986

30 R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.29147:AA883993

35 R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.3e-94:463:97//Hs.155050:AA908765

R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438

40 R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701

R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//1.1e-99:469:98//Hs.6564:U92715

45 R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636

50 R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234

R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:AI051591

55 R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941

EP 1 074 617 A2

- R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909
- 5 R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755
- R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020
- 10 R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840
- R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697
- 15 R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671
- R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270
- 20 R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952
- R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505
- 25 R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980
- R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:H47461
- 30 R-PLACE1003537//ESTs, Weakly similar to multispinning membrane protein [H.sapiens]//7.4e-69:338:98//Hs.110439:N93209
- R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321
- 35 R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591
- R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.92381:AB007956
- 40 R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264:65//Hs.158253:R86178
- 45 R-PLACE1003584
- R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542
- 50 R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459:89//Hs.23884:AD77106
- 55 R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875
- R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88//Hs.56851: